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The 12th International Epidemiology Workshop (IEW12)

Lillehammer, Norway
10 – 14 June 2018

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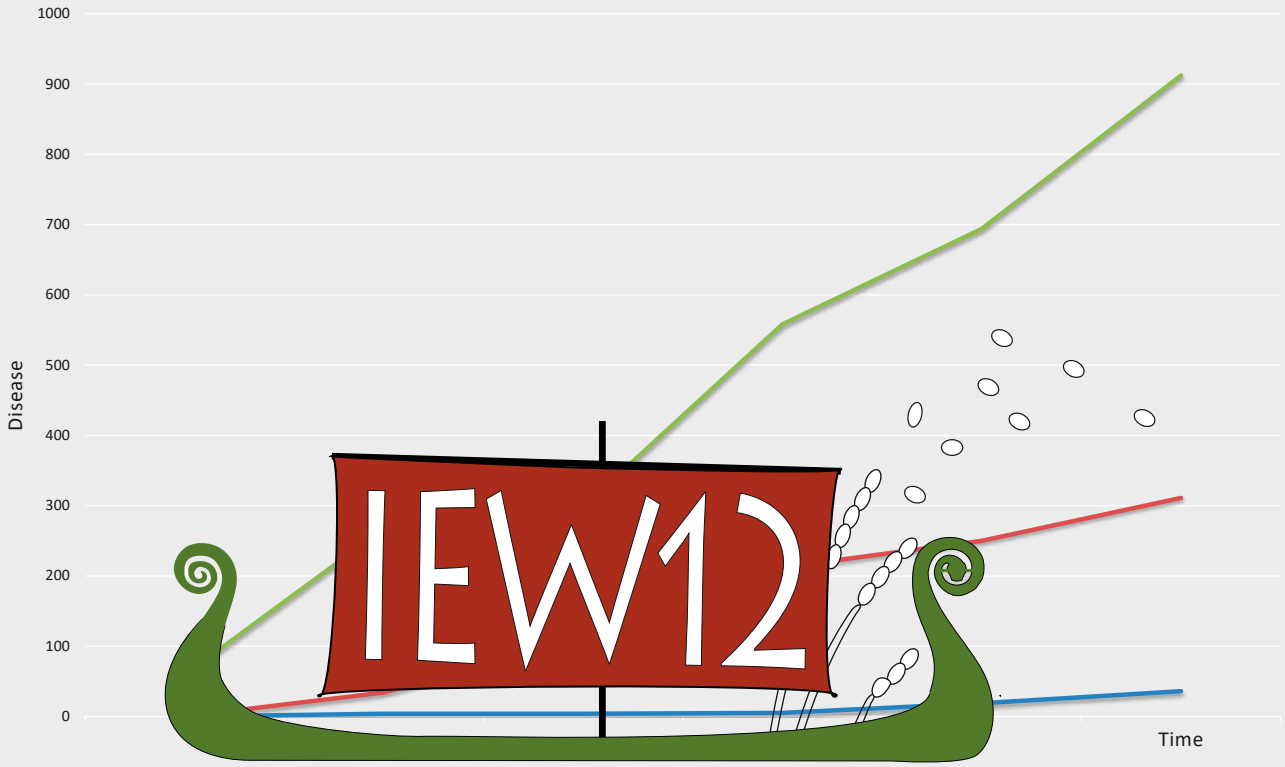

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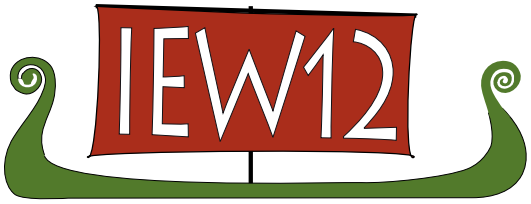

Lillehammer, Norway
10 – 14 June 2018

Preface

The 12th International Epidemiology Workshop (IEW12) takes place at Lillehammer, Norway 10 - 14 June 2018. Formal sessions are held at the Scandic Lillehammer Hotel and Conference Center. The conference organizers are Arne Stensvand, Andrea Ficke, Belachew Asalf, and Berit Nordskog of the Norwegian Institute of Bioeconomy Research (NIBIO), and David M. Gadoury of the Plant Pathology and Plant-Microbe Biology Section at Cornell University. The scientific program was developed by the foregoing, with substantial input from Larry Madden of the Ohio State University, Katherine Stevenson of the University of Georgia, and Jonathan Yuen of the Swedish University of Agricultural Sciences. The workshop is attended by registrants from 17 countries, including Australia, Brazil, Canada, China, Ireland, Israel, Italy, Japan, The Netherlands, New Zealand, Norway, Spain, Sweden, Switzerland, Taiwan, UK, and USA.

Beginning with the first International Epidemiology workshop in 1963, IEW has served as the forum for presentation and discussion of the most current research in plant disease epidemiology. We are fortunate to have among registrants of IEW12 several senior scientists who participated in the earliest workshops. The historical record of these conferences was supplemented by the many photographs supplied to the conference conveners, which have been duplicated for distribution to the registrants of IEW12.

The 51 formal presentations at the conference are divided between oral and poster format. Manuscripts prepared by the authors of the above presentations comprise this book. No distinction has been made between manuscripts prepared for oral vs. poster presentations, and they appear in the order they are presented at the meeting.

We would like to acknowledge the conference secretaries, Ellen Schei Pongo and Cathrine Lill Broch, and the website designer and manager Erling Fløistad, who is also the official photographer for the workshop. The staff at the Scandic Lillehammer Hotel have been exceptionally helpful in setting up the rooms for the meeting and dealing with the many last-minute adjustments that are a part of any such meeting. Lastly, we would like to acknowledge the conference participants themselves for volunteering to chair, moderate and facilitate the sessions and subsequent discussions.

Arne Stensvand Andrea Ficke Belachew Asalf

Berit Nordskog David Gadoury

The 12th International Epidemiology Workshop (IEW12)

PROGRAM

Sunday 10 June 2018	
14:00 – 19:00	Registration
19:00 – 21:00	Dinner and informal reception

Monday 11 June 2018

Monday 11 June 2018	
09:00 – 09:10	Welcome by Arne Hermansen, Director at NIBIO Biotechnology and Plant Health Division
09:10 – 09:15	Welcome by Jonathan Yuen, IEW Committee
09:15 – 09:20	Practical information

Oral presentations: Prediction, forecasting and decision support systems

Robert Seem/Berit Nordskog, moderators

09:20 – 09:50	Antonio Vicent: Partial receiver operating characteristic curve analysis to evaluate decision-support systems for plant disease management
09:50 – 10:10	Elisa Gonzalez Dominguez: DSSs: A tool for transferring innovation from research to practice
10:10 – 10:30	Annika Djurle: Leaf blotch diseases in barley and wheat in the Nordic - Baltic region: Occurrence and yield impact
10:30 – 10:50	Break
10:50 – 11:10	Berit Nordskog: User friendly IPM-tools for international use and local relevance
11:10 – 11:30	Lior Blank: Data driven approach for disease management
11:30 – 11:40	Arne Stensvand: Why is integration of models in disease warning a slow process?
11:40 – 12:00	Discussion
12:00 – 13:30	Lunch

Oral presentations: Control, losses, economics, interactions

Annika Djurle/Dan Anco, moderators

13:30 – 14:00	Armando Bergamin Filho: Has primary inoculum enough force of infection to cause epidemics of polycyclic diseases?
14:00 – 14:20	Björn Andersson: Fungicide treatment in winter wheat - where biology and economy meet
14:20 – 14:40	Zhanhong Ma: How epidemiological knowledge is converted into wheat stripe rust management practices in China
14:40 – 15:00	David Gadoury: Phenological heterogeneity and cold shock: Interactions with climate and epidemic progress
15:00 – 15:20	Break
15:20 – 15:40	Natalia Peres: Breaking the epidemic cycle between disease in strawberry nurseries and fruit production fields
15:40 – 16:00	Omer Frenkel: Epidemiological aspects of co-infection by viral and oomycete pathogens
16:00 – 16:20	Discussion

Monday evening from 19:00

- Dinner in the hotel garden
- Swedish Folk Music

Tuesday 12 June

Oral presentations: Measuring and assessing disease

Robert Beresford/Xiangming Xu, moderators

08:30 – 09:00	Larry Madden: Is disease severity a good surrogate for yield loss or toxin contamination?
09:00 – 09:20	Emerson Del Ponte: To diagram or not to diagram: Is there a future for diagrammatic visual severity assessments aids?
09:20 – 09:40	Kaitlin Gold: Using hyperspectral reflectance-based predictive models for early *Phytophthora infestans* detection in potato
09:40 – 10:00	Olufemi Akinsanmi: Etiology of flower blights in macadamia in Australia
10:00 – 10:20	Discussion
10:20 – 10:40	Break

Poster session 1 – brief oral presentations

David Gadoury/Belachew Asalf, moderators

10:40 – 10:45	Barbara Ludwig Navarro: Disease Efficiency: A study case with *Phakopsora euvitis* in *Vitis labrusca*
10:45 – 10:50	Kuo-Szu Chiang: Ordinal scale estimates of plant disease severity: Comparing treatments using a proportional odds model
10:50 – 10:55	Håvard Eikemo: Determining relevant factors for *Sclerotinia sclerotiorum* infections (the story of a nightmare)
10:55 – 11:00	Akira Kawaguchi: Epidemiology of *Pseudomonas syringae* isolated from barley and wheat infected with bacterial black node in Japan
11:00 – 11:05	Peter Ojiambo: Dispersal gradients of disease epidemics: How stable is the spread parameter for a power-law contact distribution?
11:05 – 11:10	Tai-Guo Liu: Population genetic structure of *Puccinia triticina* in five provinces of China
11:10 – 11:15	Antonio Nogueira: Damage of downy mildew (*Plasmopara viticola*) on grapevine *Vitis labrusca*: Virtual lesions and photosynthesis limitations
11:15 – 11:20	Armando Bergamin Filho: Amplifier hosts as main inoculum sources of primary infection for tomato begomovirus epidemics in Brazil
11:20 – 12:00	Visiting posters
12:00 – 13:30	Lunch

Special topics

13:30 – 14:10	Jonathan Yuen: Tools for modelling plant disease epidemics with R
14:10 – 14:40	Emerson Del Ponte: Open ideas, data and code sharing: Epidemiologists should be in front!
14:40 – 15:00	Discussion

Tuesday afternoon and evening, from 15:00

- Bus trip to Gjøvik
- Boat trip on the Mjøsa Lake, from Gjøvik to Lillehammer
- Dinner at the hotel

Wednesday 13 June

Oral presentations: Models, network, analysis

Peter Ojiambo/Dani Shtienberg, moderators

08:30 – 09:00	Wopke van der Werf: Pathway models for assessing the risk of invasion of plant pests and diseases; challenges and opportunities
09:00 – 09:20	Vittorio Rossi: Multi-modeling approach for IPM
09:20 – 09:40	Kelsey Andersen: Modeling epidemics in seed systems to inform management strategies
09:40 – 10:00	Robin Choudhury: Evaluating regional management strategies for avocado laurel wilt
10:00 – 10:20	Dalphy Harteveld: Machine learning for disease epidemiology of blueberry mummy berry
10:20 – 10:40	Break
10:40 – 11:00	Robert Beresford: Comparing models to predict invasive range of an unwanted organism: myrtle rust (*Austropuccinia psidii*) in New Zealand
11:00 – 11:20	Vincent Philion: Temperature response curve and distribution of the infection speed of ascospores of *Venturia inaequalis*
11:20 – 11:40	Dani Shtienberg: Aerial dissemination of *Lasiodiplodia theobromae* and *L. pseudotheobromae* pycnidiospores
11:40 – 12:00	Discussion
12:00 – 13:30	Lunch

Poster session 2 – brief oral presentations

Emerson del Ponte/Kaitlin Gold, moderators

13:30 – 13:35	Belachew Asalf: Epidemiology of post-harvest diseases of carrots in cold storage
13:35 – 13:40	Dan Anco: Assisting peanut growers in reducing harvest losses in the presence of defoliation caused by leaf spot diseases
13:40 – 13:45	Elliott Bussell: Using optimal control theory to inform disease management at the landscape scale
13:45 – 13:50	Louise Larissa May De Mio: Spatial-temporal pattern of plum leaf scald
13:50 – 13:55	Lillian Amorim: Defoliation assessment of Asian grapevine leaf rust
13:55 – 14:00	Ingerd Hofgaard: Weather conditions associated with mycotoxin accumulation in Norwegian oats
14:00 – 14:05	Tomke Musa: Epidemiological studies to improve the decision support system FusaProg
14:05 – 14:10	Xiangming Xu: Dispersal of beneficial bacteria on plant leaf surfaces under protection
14:10 – 14:15	Mladen Cucak: Revision of potato late blight risk forecasting in republic of Ireland
14:15 – 14:20	Elisa Gonzalez Dominguez: Modelling Physical Mode of Action (PhMoA) of fungicides
14:20 – 14:25	Vittorio Rossi: Incorporating host resistance in epidemiological models
14:25 – 15:30	Visiting posters

Wednesday afternoon and evening, from 15:30

- Walk to the Maihaugen Folk Park
- Norwegian Folk Dance
- Gala dinner at the Hotel

Thursday 14 June

Oral presentations: Fungicides and control

Katherine Stevenson/Natalia Peres, moderators

08:30 – 09:00	Katherine Stevenson: Predicting fungicide performance in the field from results of in vitro fungicide sensitivity assays
09:00 – 09:20	Jeff Standish: Spatial variation and temporal dynamics of fungicide sensitivity in *Venturia effusa* within a pecan orchard
09:20 – 09:40	Rodrigo Onofre: Powdery mildews in controlled environment agriculture systems: The underestimated role of light
09:40 – 10:00	Discussion
10:00 – 10:20	Break

Oral presentations: Genetics

Michael Shaw/Tai-Guo Liu, moderators

10:20 – 10:50	Michael Shaw: Discontinuities in pathogen prevalence arising from non-additive interactions between genes or environmental factors
10:50 – 11:10	Xiangming Xu: Fungal mating is not necessarily random as often assumed
11:10 – 11:30	Benjamin Watkinson-Powell: The role of spatial heterogeneity in the optimal deployment of host crop resistance genes for durable and effective disease control
11:30 – 11:50	Discussion
11:50 – 12:00	IEW business
12:00 – 13:30	Lunch

Departure

The 12th International Epidemiology Workshop (IEW12)

Content

Prediction, forecasting and decision support systems

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Measuring and assessing disease

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Models, network, analysis

Poster session 2

Fungicides and control

Genetics

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Partial receiver operating characteristic curve analysis to evaluate decision-support systems for plant disease management

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Avoiding false negatives is critical to enhance trust in decision support systems and its subsequent adoption, particularly in high value crops whose intended users are risk averse. Alternaria brown spot (ABS) is a serious fungal disease of mandarin in the Mediterranean Basin. Due to the rigorous fruit quality standards for citrus (OECD, 2010), decision support systems with high sensitivity are needed for ABS control. Experiments were conducted with the susceptible mandarin cultivars 'Fortune' and 'Nova' inoculated at different temperatures and leaf wetness durations (LWD), including interrupted periods. Disease incidence data were fitted to generalized additive models (Wood, 2006) and a generic infection model (Magarey et al., 2005). ABS incidence did not increase after an LWD interruption of 1 h on 'Nova' and 2 h on 'Fortune'. An LWD of 16 h was necessary for disease onset at the lowest temperature evaluated of 8 ºC. Models indicated an optimal temperature range between 20 and 25 ºC, but with relatively high ABS incidence also at suboptimal temperatures. Exposure of trap plants of 'Fortune' and 'Nova' in ABS-affected orchards was used for model evaluation in three locations in Valencia province, Spain, including the Alter-Rater model (Timmer et al., 2000) and a simple rule system (SRS) based on temperature and rainfall. The total area under the receiver operating characteristic (ROC) curve is a widely used index of model performance, defined as the integrated 1-specificity over all sensitivity values (Metz, 1978). Nevertheless, only those cut-off thresholds of the model yielding a low rate of false negatives are acceptable for ABS management. In these situations, the total area under the ROC curve may not be a meaningful summary of model performance and might lead to the selection of inappropriate models and/or cut-off thresholds. Instead, the partial area under the ROC curve (McClish, 1989) was used here to select models for ABS that should operate in a high-sensitivity range between 0.9 and 1. All the models evaluated for ABS had unacceptable high false positive rates on 'Fortune', resulting in unnecessary fungicide sprays. Only the SRS showed a substantial strength of agreement (Cohen's kappa = 0.63) between predictions and observations in 'Nova', with a false positive rate of 0.16 and a false negative rate of 0.07. The SRS model was implemented at http://gipcitricos.ivia.es/avisos-alternaria to improve the efficacy and efficiency of fungicide schedules for ABS control, allowing for more targeted applications. The low false negative rate obtained with this model will be decisive for its acceptance by citrus growers.

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DSSs: A tool for transferring innovation from research to practice

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An important goal in modern agricultural crop production is to develop less intensive and integrated farming systems with reduced inputs of fertilizers and pesticides and reduced use of natural resources (water, soil, energy). The transition from conventional to integrated pest management and, more in general, to integrated production requires an increase of knowledge about the farming system, with a holistic approach (Rossi et al., 2012). In Europe, the framework for IPM is the Directive 128/2009/EC on the Sustainable Use of Pesticides that makes IPM mandatory across Europe. The directive gives priority to the use of non-chemical methods and promotes low pesticide-input pest control, by the implementation of tools for pest monitoring and decision making. In this work, we present the development and use of two decision support systems (DSSs), named vite.net and grano.net, for the sustainable management of vineyards and wheat, respectively. Both DSSs are provided by Horta srl., a spin-off company of the University of Piacenza (www.horta-srl.com); they are web-based tools accessible from the company website through a username and password (7/7days, from PC, tablet or smartphone). The DSSs are structured in two main parts: i) an integrated system for real-time monitoring of the field components (air, soil, plants, pests, and diseases); and ii) a web-based tool that analyses these data by using a multi-modelling approach and then provides up-to-date information for managing the crop in the form of alerts and decision supports. The DSSs provide information about the main pests and diseases, plant growth, abiotic stresses (temperature and water), choice, application (dose and timing) and residual protection of Plant Protection Products (PPPs), and fertilisation. The decision supports and alerts provided by the DSSs are tailored to a Crop Unit (CU), which is a vineyard or a wheat field managed in a uniform manner all season long. Each CU is characterized by means of site-specific information both static (i.e., do not change over the season and are provided by the user to the DSS) and dynamic (i.e., change over the season), which represent the input variables of the models running within the system. To develop these DSSs, Horta used a well-established approach that aims at overcoming the so-called "problem of implementation" of DSSs for agriculture: i) mathematical models present in the DSSs are developed and validated "in house" by the researchers of Università Cattolica del Sacro Cuore and others; ii) once implemented, the DSS is experimentally evaluated by researchers and practically evaluated by farmers in pilot farms; iii) end users are involved during the development of the DSS (to ensure that their needs are met), and during its evaluation and final use (to understand their DSS's acceptance and to obtain continuous feed-backs about weaknesses and strengths of the DSS). In season 2017, 3.500 farmers used grano.net® in order to produce > 270.000 tons of grain on about 30.000 ha, and 300 farmers used vite.net® on approximately 12.000 ha across Italy. The use of the DSSs significantly increase the farmer's profit and decrease the environmental impact of crop production. For instance, the use of vite.net reduced by 37 % in average the use of fungicides on grapevine, and the use of grano.net decreased by 10 % in average the carbon footprint of wheat production.

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Leaf blotch diseases in barley and wheat in the Nordic – Baltic region: Occurrence and yield impact

Marja Jalli[1], Timo Kaukoranta[1], Janne Kaseva[1], Björn Andersson[2], Andrea Ficke[3], Lise Nistrup-Jørgensen[4], Antanas Ronis[5], Annika Djurle[2]

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Three leaf blotch diseases in wheat, septoria tritici blotch, tan spot, and stagonospora nodorum blotch (acronyms: STB, PTR, SNB), are largely considered as chronic diseases in the Nordic – Baltic region. In barley, the most common leaf blotch diseases in the area are net blotch and scald. There is a wide variation in incidence and severity of these diseases between years and cultivation areas. The variation is related to climatic conditions and cultivation history and methods. Fungicides are used as an acute control measure when preventive actions have been insufficient to maintain disease severities at levels that are acceptable to the grower. The use of fungicides varies in the region, with a higher frequency of treatments in the southern areas and a lower frequency further north. While in some areas the main questions relates to the number of treatments, doses and timings, other areas might not need to apply fungicides at all. The ongoing research project Spot-IT (IT-solutions for user friendly IPM-tools in management of leaf spot diseases in cereals, 2017 - 2020) aims to provide cereal farmers with better models for predicting leaf blotch diseases in wheat and barley. In this study, data from past fungicide efficacy field trials from Denmark, Finland, Lithuania, Norway and Sweden were compiled and analysed in order to produce a comprehensive record of correlations between disease progress, and yield losses in the Nordic – Baltic region. The data was collected in 2006-2017 from spring barley, winter wheat (Denmark, Lithuania, Sweden) and spring wheat (Finland, Norway). The aim of our project is to use this information and knowledge to increase the understanding of leaf blotch diseases in cereal production in the Nordic-Baltic region and to define the economic thresholds for disease management and decision support on a multi-national level. The first results from the analysis will be presented.

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User friendly IPM-tools for international use and local relevance

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Models for prediction of pests and diseases are important tools for decision support in integrated pest management (IPM). In Norway, the freely available service VIPS (www.vips-landbruk.no) is an online forecasting system made for this purpose. The VIPS is Open Source, made for international collaboration, and allows for local adaptations, incorporation of models and other services. To encourage and increase local use of decision support systems, user needs have to be identified to understand the best approach for the selection of relevant models and the presentation of data. As part of the ongoing research project SpotIT (IT-solutions for user friendly IPM-tools in management of leaf spot diseases in cereals, 2017 - 2020), VIPS will be used to coordinate model outputs for leaf blotch diseases in barley and wheat from Nordic-Baltic countries (Norway, Sweden, Finland, Denmark, Lithuania). Model outputs from VIPS will also be integrated with farm-scale ICT infrastructure platforms, such as the Finnish CropInfra. User interactions will provide important information on how to meet the local expectations to model outputs and presentation formats, and each partner country will select relevant input for their DSS or platform. In the Norwegian VIPS web, model outputs are based on data from a network of weather stations (AgroMet Norway, lmt.nibio.no) and weather forecasts from the Norwegian Meteorology Institute. However, there is a demand for more local and field-related input data. To adapt model outputs to a wider geographical area, and a wider range of users, new ways of visualizing risk model outputs are under development. This includes an extended use of gridded weather data to improve the local relevance at the field level. Preliminary results will be presented, and the potential and limitations in use of weather data from different sources will be discussed, using perspectives from the model developer, weather data provider and advisor/farmer.

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Data driven approach for disease management

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The "classical" research approach is based on testing hypotheses related to variables affecting phenomena under study, using experimental methods. The main drawback of this approach is the need to focus on the effects of only one or a limited number of variables. In addition, in most cases the study is limited in space and time. An alternative methodology is the "data driven" approach (Michener & Jones, 2012). In this approach, a phenomena under study will be examined within the biological system and a large number of variables can be analyzed, without the need to select only few. According to this approach, numerous observations collected from commercial agricultural plots are analyzed along with geographical, environmental and meteorological data. Increase in the availability of geospatial data and rich environmental databases provide new sources of valuable information for landscape-scale research. This enables characterizing the factors affecting disease development over space and time. The advantages of data driven studies are described herein for two case studies: the former successfully identified the variable affecting disease outbreak, and in the latter we generated a weather-based mathematical model that quantifies the spatial dynamics of a disease. Both resulted with an output that contribute to disease management. *The first case study focused on Clavibacter michiganensis* subsp*. michiganensis*, the causal agent of bacterial canker and wilt of tomato (Blank et al., 2016). Data from 681 commercial production units (greenhouses and net-houses) were analyzed. The results suggested an absence of anisotropy pattern in the study region and that disease severity had significant spatial autocorrelation. The strongest spatial autocorrelation occurred within a 1500 m neighborhood which is comparable to the distance between production units maintained by one grower. The group of variables explaining the largest proportion of the variation was related to disease development during the growing season. This helped to identify the main cause of disease outbreak—handling plants while the leaves bear guttation droplets (Sharabani et al., 2013). In the second case study we used data on dozens of potato fields over four growing seasons to model the spread of late blight at a regional scale (Firester et al., 2018). The model was validated with an independent data set and then used to create risk maps showing the likelihood of future outbreaks in the region. The risk maps can be used by growers to optimize late blight managment by alerting them to the most probable day on which their fields are at the highest risk, using real-time weather data. These risk maps can be updated daily to account for conditions needed for sporulation, sporangia spread and infection. These case studies highlight the benefit of using the „data driven" approach, and in particular the use of data from commercial plots, to complement the traditional, experimental approach.

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Why is integration of models in disease warning a slow process?

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Despite extensive publication of studies in the leading peer-reviewed journals of a profession, the incorporation of new information on pathogen biology, pathogen ecology, host resistance, and disease management can proceed at a maddeningly slow pace. This can be especially true when biological results challenge long-standing commercial practices, or long-established recommendations for a particular pathosystem. The *Venturia inaequalis*/apple scab pathosystem is one of the best examples that research can outpace the recommendations of a broad sampling of IPM programs worldwide, and the consequent commercial disease management practices. For example, the original Mills infection period table for apple scab never underwent peer review, nor was the foundational data upon which it was based ever published. It represented a major advancement in disease management for its time (the 1940s), and it is still in use today. In fact, the original table is presently listed in the chapter on apple scab in the most recent APS Compendium of Apple Diseases. Nonetheless, papers published both prior to and after Mills clearly demonstrated several flaws in the original Mills Table. Examples of the slow adoption (and even non-adoption) of research findings can also be found with respect to the role of chasmothecia as primary inoculum in powdery mildews of grapevine, strawberry, and hops; in the development of organ-specific ontogenic resistance in diverse fruit crops; in the importance of absolute inoculum potential in polycyclic pathogens; etc. Several hypotheses are presented for discussion with respect to the foregoing situation. Slow adoption may reflect a disconnect between the research community and the outreach/advisory community beyond a local level. In other words, research discoveries are published internationally, but their most effective advocates (the authors) act best in local or regional settings. There may be a natural tendency of experts and experienced end users of a system to doubt the value of change, in particular when change is perceived as being accompanied by risk. Original authors may act upon the belief that the value of a discovery is self-evident, and do not participate in local verification or implementation. In fact, they may view such work as disbelief of their findings.

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Has primary inoculum enough force of infection to cause epidemics of polycyclic diseases?

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In high input agricultural crops, some polycyclic diseases vectored by insects can behave as monocyclic because secondary dissemination is suppressed by frequent insecticide sprays (Bergamin Filho et al., 2016). Huanglongbing of citrus (two sprays per month) and begomovirus of tomato (three sprays per week) are good examples. For huanglongbing the structure of the epidemic is well understood; primary infections occur continuously during the growing season, neighboring older citrus orchards being the principal source of primary inoculum. Area-wide management in citrus orchards, although difficult to implement, can prevent epidemics (Bassanezi et al., 2013). The situation is not so simple for begomovirus of tomato. Populations of several species of weeds are the pathogen's reservoir (Barreto et al., 2013), but we do not consider that these populations have enough force of infection (*sensu* Viana et al., 2014) to drive epidemics in absence of secondary dissemination. Despite this, severe epidemics are recurrent (Macedo et al., 2017). We propose the existence in the agroecosystem, in some places and time, of amplifier hosts that provide the necessary force of infection for epidemics to occur; amplifier hosts are ideally asymptomatic, occur in high density near the target host, and supports growth of both virus and vector (Bergamin Filho et al., 2018 – this conference). In the Brazilian tomato agroecosystem amplifier hosts are soybean and, possibly, common bean. The concept of amplifier hosts applied to botanical epidemiology can have profound consequences for the understanding and management of several pathosystems, especially vectored diseases in tropical and subtropical agriculture.

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Fungicide treatment in winter wheat – where biology and economy meet

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The economic return from fungicide treatments varies between fields and years. This makes it hard to make correct decisions on the need of fungicide application in each individual situation. Better-informed decisions are needed to direct the use of fungicides to situations when it is both biologically and economically justified. This is a corner stone for integrated pest management and essential for the growers' long-term economic return. Without tools that can capture the variability of the need for treatment at a satisfactory level, there is a risk that fungicides will be used with less attention to the actual need, and even routinely applied. There are several methods for identifying risk factors that contribute to plant disease epidemics, or yield losses (amount or quality) caused by plant pathogens. Logistic regression is an objective method that allows for the identification of both continuous and categorical factors, and their quantification both as single factors and several factors combined. Historical data is a good source of information, but there are limitations in how it can be validated and how results can be interpreted for agricultural systems that constantly change. We used logistic regression to analyse the marginal return of fungicide treatments against leaf blotch diseases in winter wheat fields in Sweden by comparing yield increases from fungicide treatments with data on growing conditions (historical field and weather data). We will discuss problems that were met during data analysis, and when newer data was used for validation.

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How epidemiological knowledge is converted into wheat stripe rust management practices in China

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Wheat stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*), is the most devastating wheat disease in China. Wheat stripe rust in China demonstrated unique features in inter-regional epidemics, and the disease spread over large geographical regions mainly via pathogen long-distance dispersal. Three main epidemic regions (oversummering, overwintering, and spring epidemic regions) were identified on the basis of surveys over a large geographical range, long-term monitoring of the disease progress at selected locations combined with geographic information system, and DNA fingerprint analysis. However, in northwestern China, one of the most important oversummering regions for *PSt*, is considered as the core inoculum source, and the relationship between inoculum in this region and adjacent wheat-growing regions revealed that the Gansu and Ningxia provinces play an important role in the disease cycle and long-distance dispersal. Spore trapping in 2013-2015 in Gansu Province also proved that *Pst* was present during the whole year, and such trapping provide an efficient method to monitor the dynamic of airborne spores of *Pst* and forecast the disease spread. For the latent period of wheat stripe rust, molecular disease index (MDI) was put forward, and the quantity of inoculum during the latent period could be used for forecasting disease based on the relationship between MDI and DI (disease index). It was revealed that the emerge and production of new highly pathogenic races was the main reason for the resistance loss in wheat varieties. A regional management strategy was proposed, and different strategies was implemented to corresponding oversummering, overwintering and spring epidemic regions.

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Phenological heterogeneity and cold shock: Interactions with climate and epidemic progress

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Despite inherent simplifications, if models in advisory systems result in more efficient disease suppression, then all is well. However, there are indirect effects of climate upon pathosystems that can cause advisory systems to inexplicably underperform or even fail. The risk is maximized as climate changes, or as production of a crop expands to areas with climates that are, from an evolutionary perspective, unfamiliar to the host and/or pathogen. We investigated two such phenomena: (i) climate-based phenological heterogeneity; and (ii) modification of host susceptibility by acute overnight cold events. Climate-based phenological heterogeneity is distinct from minimum chilling requirements of perennial crops. Very little is known of how degree and depth of winter chilling affects *synchronization* of host regrowth upon emergence from dormancy. We studied interactions between chilling, asynchronous phenology, development of ontogenic resistance, and the consequent risk of disease in grapevine. In a global study, mean temperature of the three winter months ranged from -4.1 to 11.8 °C among 15 sites on 3 continents, and was associated with duration of bloom at each site: 2 d at the coldest sites, and > 2 wks at the warmest sites. This 7-fold increase in duration of bloom translated to protracted susceptibility due to delayed development of ontogenic resistance to *Erysiphe necator* and *Plasmopara viticola*. Downstream effects of asynchronous bloom included asynchronous ripening and sugar accumulation. Climate-based asynchrony in certain fruit crops may increase the risk of disease in pathosystems typified by phenology-defined windows of susceptibility. Bloom duration can be used to quantify impact of winter chilling on asynchronous penology, and once quantified, the impact of climate change can be projected by examining these interactions across existing climatic gradients. Regarding effects of acute cold: pathogen development has been extensively studied with a primary focus on cardinal temperatures. Less is known regarding effects of acute cold (> O °C and < 8 °C) on pathogen development as mediated by temperature-modified host resistance. Biotrophic pathogens in particular can be sensitive to even transient stress to the host, including cold-induced stress that has no direct effect upon the pathogen. *Erysiphe necator* was adversely affected by pretreatment of susceptible grape leaf tissue by exposure to 2 °C to 8 °C for 2 to 8 h. Acute cold that proceeded inoculation reduced infection efficiency. Colony expansion was reduced when tissues were later inoculated. Nascent colonies exposed to acute cold exhibited hyphal mortality, reduced expansion, and increased latent periods. Observed weather and consequent radiational cooling plants indicated that cold events capable of inducing the foregoing responses occur commonly across most viticultural regions worldwide. These phenomena may partially explain (i) the stalling of foliar epidemics of grapevine powdery mildew during the first month after budbreak, and (ii) the sudden increase in epidemic development once seasonal temperatures increase above the threshold for acute cold events. The foregoing effects of acute cold have been more recently demonstrated in powdery mildews of *Arabidopsis* and hops, the latter of which exhibits a "stalled" epidemic similar to that observed on grapes.

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Breaking the epidemic cycle between disease in strawberry nurseries and fruit production fields

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Clean planting stock is the foundation of an effective disease management program. For strawberry, producing clean planting stock is a challenge because transplants are produced remotely from fruit production sites under different growing conditions and climates. Recently, there has been a preponderance of evidence showing that many pathogens such as *Colletotrichum acutatum* (Ureña-Padilla et al. 2001), *Botrytis cinerea* (Oliveira et al. 2017), *Phytophthora cactorum* (Browne and Bhat 2011), *Podosphaera aphanis*, and *Xanthomonas fragariae* (Maas et al. 1995) are harbored on transplants from nurseries. Because the same limited groups of fungicides are often used in both nurseries and fruit production fields for managing diseases, fungicide resistance is a major problem. This is particularly evident in fruit production fields where essentially the last round of plants from a multi-year propagation cycle are planted. The lack of non-chemical alternatives, and the use of resistance-prone fungicide in nurseries sets the stage for the downstream problems experienced in fruit production fields. A thermotherapy protocol that relies on aerated steam (44 °C for 4 h) and a pre-heat treatment step (37 °C for 1 h) to condition plants was developed to eradicate bacterial and fungal pathogens from strawberry transplants. The use of aerated steam rather than hot water immersions reduces the risk of spreading microbial and nematode pathogens in treated batches. In numerous field trials, it was shown that aerated steam was less damaging to plants than hot water dipping. The aerated steam treatment was proven effective in reducing *X. fragariae* (Turechek & Peres, 2009), *C. acutatum* (Wang et al., 2017) as well as multi-fungicide resistant populations of *B. cinerea* (Zuniga et al., 2017) on strawberry transplants. Preliminary results have also shown great potential for reduction of *P. cactorum*, including newly emerged isolates resistant to mefenoxam. In summary, thermotherapy treatment using aerated steam has great potential to serve as a non-chemical tool for general disease management and for nurseries to reduce fungicide resistant populations from their planting stock.

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Epidemiological aspects of co-infection by viral and oomycete pathogens

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Plant pathology studies are mainly focused on one host/one pathogen paradigm, but several pathosystems also involve co-infection by several pathogen species (Abdullah et al., 2017). Co-infection may result in symptoms that are dissimilar from those of infections by each of the pathogens alone and may even increase the damage to the host. In this report, we describe the synergistic effect of co-infection by *Cucumber green mottle mosaic virus* (CGMMV) and *Pythium* spp. In the last decade, the phenomenon of late-wilting has increased in cucumber greenhouses during CGMMV outbreaks. As wilting appears in defined patches accompanied by root rot, it was hypothesized that the phenomenon is caused by co-infection of soilborne pathogen/s and CGMMV. A field survey showed that 69 % of the wilting plants were colonized simultaneously by *Pythium* spp. and CGMMV, whereas only 20 and 6.6 % of the wilting plants were colonized only with *Pythium* spp. or CGMMV, respectively. Artificial inoculation of cucumber plants revealed that co-infection with *P. spinosum* and CGMMV leads to a significant synergistic wilting effect and reduced growth parameters (Philosoph et al., 2018). The synergy values of the wilting effect were not influenced by the time interval between *P. spinosum* and CGMMV infection. However, dry-mass synergy values were decreased with longer intervals between infections. Furthermore, it was found that co-infection by *Pythium* spp. and CGMMV occur during the whole year, but during the summer months *P. aphanidermatum* rather than *P. spinosum* was more common. The former favors higher temperatures than the latter (Al-Sa'di et al., 2007). Nevertheless the synergistic effect of co-infection with CGMMV was common for both *Pythium* species. Results of this study demonstrate the complexity of pathosystems involving co-infections by two (or more) pathogens. They encourage a wider perspective of the complexity of agricultural diseases to apply the most suitable disease management.

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Is disease intensity a good surrogate for yield loss or toxin contamination?

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Plant disease epidemiologists routinely assess disease intensity (e.g., incidence or severity) in order to characterize temporal and spatial dynamics of epidemics, evaluate control treatments, and predict yield loss or the toxin levels in the harvested products of the crop. In the latter situations, disease intensity (assessed at a single time or AUDPC) could be considered a surrogate for yield or toxin. The concept of surrogacy is uncommon in plant pathology, but is well established in medicine and in some other biological fields. According to Buyse et al. (2000), "a surrogate endpoint [response variable] is one which can be used in lieu of the endpoint [response variable] of primary interest in the evaluation of experimental treatments or other interventions". Surrogates are valuable if they can be measured earlier, more frequently, more conveniently, or more cheaply than the variable of primary interest. Disease intensity is certainly measured earlier than yield or toxin concentration, and may fit the other conditions in many circumstances. In order to be used as a surrogate, the variable must be validated, usually in a collection of trials with meta-analytical methods. Surrogates can be utilized at two different levels. Individual-level surrogacy corresponds to the situation where one can predict the variable of interest using another variable in individual experimental or sampling units (e.g., plants, plots, fields). This would be useful to possibly prescribe a control treatment for that unit. Trial-level surrogacy corresponds to the situation where one can predict the effect of a treatment (e.g., fungicide) on the variable of interest, based on the effect of the treatment on the surrogate variable. For instance, if one has an estimate of the difference in mean disease intensity between the control and treatment, then one can predict the difference in mean yield between the control and treatment. A given potential surrogate may be useful at the individual or trial level, or both. Both individual-level and trial-level surrogacy can be evaluated and validated when one has: 1) a collection of trials with two (or more) treatments of interest (control and the treatment); 2) measurements of the surrogate (S) and the so-called true (T) response in the individual experimental units (plots, etc.) for all treatments in each trial. Bivariate mixed-effects models can be used to test for surrogacy, using random effects for the trial and treatment, with correlations within experimental unit between S and T, and between-trial correlations for the trial and treatment effects. We utilized the mixed-model approach to evaluate "field disease severity" (i.e., disease index) as a surrogate for yield and deoxynivalenol (DON) toxin concentration in harvested wheat grain for the Fusarium head blight (FHB) system. FHB index is routinely used to evaluate breeding lines, new cultivars, and fungicide or other treatments, although the primary interest is in yield and especially DON. Using the data from 82 trials collected as part of the FHB uniform fungicide trials (UFTs) in the U.S., we determined that index is generally not a good surrogate for DON, but possibly a moderately acceptable surrogate for yield. The statistical modeling and analysis, together with some approximations and summary measures of surrogate validity, such as trial- and individual-R-squared statistics, will be explained in the presentation.

To diagram or not to diagram: Is there a future for diagrammatic visual severity assessments aids?

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Disease quantification is a key research area in plant disease epidemiology. Methods are developed and tested for improving accuracy and reliability of disease data. Data on the symptomatic area (i.e. severity) can be obtained by several means depending on research goals, organ assessed, spatial scale, and available technology. Conceptually, severity is a ratio and, as such, it depends on two measures: total and diseased area, which must be clearly defined. Symptoms vary with pathosystem and plant organ affected. Therefore, methods should be suitable and adapted to the specific situation and the objectives of the research. In spite of the advances in remote sensing (Bock et al., 2010a), disease severity data are mainly obtained visually; hence the need to ensure that estimates are as accurate as possible mainly due to the difficulties associated with percentage severity estimation (Bock et al., 2017). Methods have been proposed to categorize severity to a limited number of ordinal scores following intervals (often logarithmic) of the percentage ratio scale. However, depending on the scale structure, errors of the estimates (when compared to the actual values) compromise precision and inferences from experiments using these scales (Bock et al., 2010b). Standard area diagrams (SADs) have long been used as an aid to improve accuracy of visual estimates of severity using the percentage scale. Advances in technology for image acquisition and analysis have led to the development of numerous SADs. Recently, we systematically reviewed trends in methods for developing and testing over 100 SADs published in peer-reviewed articles since the 1990s. The review provided a clear and unambiguous account of the current status, trends and advances and potential future direction for research to improve SAD technology (Del Ponte et al., 2017). We expand on the analysis of accuracy-related data gathered from these articles with the goal of summarizing, using meta-analytic models, the gains in accuracy and to identify factors that explain the variability in effectiveness of SADs. We will present new research and applications for SADs, including an online database and tablet/smartphone-based systems (Pethybridge & Nelson, 2017) that are moving the technology to a new paradigm for aiding visual severity estimates.

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Using hyperspectral reflectance-based predictive models for early *Phytophthora infestans* detection in potato

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Late blight of tomato and potato caused by the oomycete pathogen *Phytophthora infestans* continues to be one of the most challenging diseases to manage sustainably and proactively. Advanced field-based methods of late blight detection that can identify infection before the onset of visual symptoms would improve management by greatly reducing disease potential and spread. The objective of this work was to explore the detection of late blight infection during its latent, or biotrophic phase, using reflectance spectroscopy. We conducted controlled experiments in growth chambers using inoculated and control, non-inoculated plants to test the ability of reflectance spectroscopy for non-visual detection of infection. We measured continuous visible to shortwave infrared reflectance (400-2500 nm) on leaves of the plants using a portable spectrometer with contact probe at 12 – 24 h intervals. Our results indicated that we could detect late blight infection, caused by clonal lineages US-23 and US-08, with 80 % accuracy at just 24 h post-inoculation, and upwards of 85 % accuracy across all time points. Shortwave infrared wavelengths (>1300 nm) proved to be important for disease detection and distinguishing between the pathogen life stages of early infection, biotrophic growth, necrotrophic growth, and sporulation. Late blight infection was accurately detected up to four days before visual symptoms appeared, indicating potential for using spectroscopy as a tool for rapid, early detection of late blight in real-time.

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Etiology of flower blights in macadamia in Australia

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Macadamia nut is grown in commercial plantations in tropical and subtropical frost-free regions worldwide. Macadamia flowers are borne on pendant-like inflorescence (raceme) and develop through four stages, over 3-4 months. In the final stage of flowering, the sepals fall off and the fertilised embryos develop rapidly on the rachis. Poor fruit set, following good flowering, have been reported in many plantations in all macadamia producing regions. Various pathogens belonging to different classes of fungi and oomycetes have been reported to affect macadamia racemes. Diseases they cause are known as raceme blight, dry flower, grey mould, or blossom blight caused by *Botrytis cinerea* (Zentmyer, 1962; Holtzmann, 1963; Hunter et al., 1972; Nagao & Hirae, 1992; Mayers, 1993), *Phytophthora capsici* (Kunimoto et al., 1976; Aragaki & Uchida, 1980), *Cladosporium cladosporioides*, *Pestalotiopsis* and *Neopestalotiopsis macadamiae* (Akinsanmi et al., 2016). Studies on the epidemiology of three economically important diseases; Botrytis blight (*B. cinerea*), Pestalotiopsis blight (*Pestalotiopsis* and *N. macadamiae*) and Cladosporium blight (*C. cladosporioides*), show contrasting life cycles, which depending on weather conditions and developmental stage of the racemes, offer new insights into when each of the three diseases are likely to ocur and cause severe damage to macadamia flowers.

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Disease Efficiency: A study case with *Phakopsora euvitis* in *Vitis labrusca*

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Disease efficiency (DE) is an important parameter for comparative epidemiology, assessment of plant resistance and modelling epidemics. DE involves several monocycle components such as spore deposition, infection colonization, and reproduction. DE has been evaluated by different methods and described by different definitions. Usually, DE is referred to as infection efficiency (Lalancette et al., 1987; Sache & Zadoks, 1995; Vallavieille-Pope et al., 1995, 2018). The objective of this work was to discuss the concept and to compare different methods of measuring DE using Grapevine rust, the pathosystem *Phakopsora euvitis* - *Vitis labrusca* as a study case. The definition of Kranz (1996), i.e., disease efficiency is the number of lesions divided by the number of spores deposited over plant tissue surface, is proposed to standardize the concept of DE. Furthermore, as proposed by Kranz, infection efficiency (IE) is defined by the number of infections per number of spores deposited over plant tissue. The difference between these concepts is due to the fact that an infection will not necessarily develop into a lesion. Grapevine rust DE was evaluated at different temperatures, leaf wetness period and inoculum concentration. Inoculations were performed in a defined leaf area of 12 cm^2. DE was calculated with data of viable spores (proportion of germinated spores at different temperatures × total number of spores in the inoculum) and with total number of spores in inoculum suspension. Data of *P. euvitis* DE at the temperatures of 15, 20, 25, or 30 °C and wetness periods of 6, 12, 18, or 24 h, estimated with the number of lesions divided by the number of viable spores at 25 °C, was best fitted to the beta-monomolecular model. The maximum value of *P. euvitis* DE, estimated to 0.22 lesions/viable spore by the beta-monomolecular model, was obtained at 24 °C and a wetness period of 24 h. The maximum DE (0.43 lesions/viable spore) was obtained using 70 viable spores per cm^2 at 25 °C. The increase of inoculum concentration of *P. euvitis* decreased DE because the infection site was limited.

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Ordinal scale estimates of plant disease severity: comparing treatments using a proportional odds model

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Studies in plant pathology and plant breeding requiring disease severity assessments often use a certain type of ordinal scale based on defined numeric ranges, which can be termed a quantitative ordinal scale. With plant disease this special form of the ordinal scale is generally based on the percent area with symptoms [e.g. the Horsfall-Barratt (H-B) scale]. We used a parametric proportional odds model to analyze directly the ratings obtained from disease scales, without converting ratings to percentages based on class midpoints of quantitative ordinal scales (currently a standard procedure). This useful feature of the model also renders it amenable to comparing estimates from studies using different response scales. The purpose of this study is to evaluate the performance of the proportional odds model for the purpose of comparing treatments (e.g. varieties, fungicides, etc.) based on ordinal estimates of disease severity. A simulation method was implemented to perform the study. The parameters of the simulation were estimated using actual disease severity data from the field. The proportional odds model was compared with the model using midpoint conversions of ordinal intervals. The criterion for comparison was the power of the hypothesis test. Our results show that the performance of the proportional odds model is never inferior to using the midpoint of the severity range at severity ≤ 50 %. Especially at low disease severity (≤ 10 %), the proportional odds model is clearly superior to the midpoint conversion of the interval method. Thus, for early onset of disease (i.e. low severities), the proportional odds model is preferable for analyzing quantitative disease severity estimation data based on ordinal scales when comparing treatments.

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Determining relevant factors for *Sclerotinia sclerotiorum* infections (the story of a nightmare)

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Sclerotinia sclerotiorum is an ubiquitous fungus attacking a multitude of important food crops (Boland & Hall, 1994). Field data from Norwegian oilseed trials showed a sporadic, but nonetheless severe attack of *S. sclerotiorum* in some years making routine spraying against this pathogen not economical. Leafy vegetables on the other hand appear to experience severe losses regularly due to this pathogen in some regions, demanding high and frequent fungicide input. The pathogen appears to depend on easily accessible nutrient sources, as its ascospores are unable to penetrate stems or leaves with thick layers of wax directly (Jamaux et al., 1995). Infection experiments in the greenhouses repeatedly failed with ascospores as inoculum source and are often done via mycelial plugs in published experiments, which poorly represent the true infection pathway. In the field, mostly ascospores initiate infection in this monocyclic disease. Even inoculation of lettuce plants with high concentrations of ascospore suspensions (10^6 spores/ml) under high humidity resulted in poor colonization of the host. In order to better understand the epidemiology of this pathogen, we explored the key stages in its lifecycle: Sclerotia survival, germination and ascospore discharge events, the humidity requirements for the infection process and the precipitation pattern associated with disease severity in the field. Our preliminary results showed that sclerotia not only survived over several years in the soil, but that they were able to discharge repeatedly through the season and over several years. In addition, we found that *S. sclerotiorum* ascospores required relative humidity above 84% to infect flower petals of oilseed plants, and that they survived under dry conditions for over three weeks on inert surfaces. Precipitation was poorly correlated with sclerotinia white rot in oilseed rape fields, and it is assumed that precipitation patterns do not reflect the relative humidity conditions in the oilseed plant canopy well enough to predict successful infection events.

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Epidemiology of *Pseudomonas syringae* isolated from barley and wheat infected with bacterial black node in Japan

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Bacterial black node caused by *Pseudomonas syringae* pv. *syringae* (PSS) is the most serious bacterial disease of barley and wheat in Japan. A repetitive sequence-based (rep)-polymerase chain reaction (PCR) and inter-simple sequence repeat (ISSR)-PCR were used to investigate the molecular typing of PSS strains isolated from barley and wheat plants with bacterial black node symptoms grown in 22 different locations and six different seed-production districts in Japan. Eighteen genomic fingerprinting (GF) genotypes were obtained from the combined results of BOX-, REP-, and GTG_5-PCR, indicating that the PSS population in Japan has high genetic diversity. The result based on logistic regression indicated that the population of GF genotype A was significantly related to a seed-producing district and that the epidemic of PSS strains in fields originated mainly from seed infection. This study will be applicable to future studies of the molecular epidemiology of bacterial plant diseases that have multiple infection routes. Also, the spatiotemporal distribution of barley and wheat plants infected with bacterial black node in fields in 2016–2017 was analyzed using Taylor's model and Iwao's model. In Taylor's model, the sample variance (s^2) of the total and the newly diseased plants at each observation increased with mean plant density (m). In Iwao's model, although the mean crowding (m^*) of total and newly recognized diseased plants increased with m, Taylor's model fit the data better than did Iwao's model. Thus, bacterial black node could be explained as a colony expansion model.

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Dispersal gradients of disease epidemics: How stable is the spread parameter for a power-law contact distribution?

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Understanding processes and factors that affect biological invasions on a landscape scale is important in establishing and predicting the risk of biological invasions. Examining these processes is thus useful in planning and designing effective measures to eradicate and contain biological invasions (Zadoks & Van den Bosch, 1994). The contact distribution is an important determinant of the velocity of spread of disease epidemics. It establishes the probability of an infectious unit originating from a given source coming into contact with a host at some distance away from the same source (Aylor, 2003; Madden et al., 2007). Long-distance aerially dispersed pathogens have a contact distribution that is typically described by a power-law model (Ferrandino, 1993). Experimental evidence indicates that such pathogens will result in epidemics with accelerating velocity of spread. The value for the spread parameter of the power-law contact distribution has been shown to be approximately 2 in several plant and animal systems (Mundt et al., 2009). However, the stability of the spread parameter over several realizations of an epidemic has not be established. We examined the stability of this parameter using outbreaks of cucurbit downy mildew in the eastern United States from 2008 to 2014. Disease outbreaks were analyzed using a spatio-temporal model of disease spread that incorporates logistic growth in time with a power law function for pathogen dispersal (Jeger, 1983). As expected, the position of the epidemic wave-front became exponentially more distant with time, and epidemic velocity increased linearly with distance. However, estimates of the spread parameter varied widely across epidemic years, with values ranging from 1.51 to 4.16. In addition, there was a significant ($P < 0.05$) interaction between the spread parameter and time (or distance) even in epidemic years where data were well described by the power-law model. The latter indicates that the spread parameter may not be expected to be stable over epidemic years and a value of 2 should be considered as the lower limit indicator of the distance of the epidemic wave front from an initial focus per unit time for pathogens whose contact distributions follow the power law model.

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Population genetic structure of *Puccinia triticina* in five provinces of China

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To explore evolution and propagation of *Puccinia triticina*, and speculate about its inoculum sources, we used single nucleotide polymorphisms (SNPs) to evaluate the *P. triticina* population genetic structure in five Chinese provinces, Gansu, Henan, Hubei, Shanxi and Sichuan, between 2013 and 2015. The results of the genetic diversity analysis showed that the populations exhibited characteristics of abundant genetic diversity, high haplotype diversity and low nuclear diversity. The analysis of gene flow revealed that extensive exchange occurred and that the *Nm* of the Gansu/Henan, Sichuan/Henan, Sichuan/Gansu populations was most frequent. And the genetic differentiation coefficient showed that genetic differentiation is significant among populations except Henan/Gansu and Henan/Sichuan ($P < 0.05$). By using S_{nn} of Hudson, Structure software and haplotype networks, we found that wheat leaf rust isolates can be subdivided into two clusters: Gansu/Henan/Shanxi/Sichuan and Hubei clusters. AMOVA analysis showed that the populations exhibit genetic variation; the variation percentage reached 87.5, and the genetic variation within populations was the major source of variation. Our results suggest that the genetic diversity of wheat leaf rust was abundant and that gene flow was frequent between populations. The five populations may have a common ancestor. However, *P. triticina* of China had experienced a rapid expansion, which caused some differences between populations. So the Hubei population was different from other populations due to genetic variation within populations.

Damage of downy mildew (*Plasmopara viticola*) on grapevine *Vitis labrusca*: Virtual lesions and photosynthesis limitations

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Downy mildew caused by the oomycete *Plasmopara viticola* is the most destructive disease of grapevine. European grapevines (*Vitis vinifera*) are highly susceptible to *P. viticola*, and American cultivars, originating from *Vitis labrusca*, *V. riparia,* and *V. rupestris* are less susceptible. However, the level of susceptibility to downy mildew differs in cultivars originating from *V. labrusca*. Some *V. labrusca* cultivars, as table cv. Niagara Rosada, are susceptible to *P. viticola.* In southeast Brazil, downy mildew is one of the major problems in the production of table grapevine. However, studies on the damage mechanisms of *P. viticola* on the physiology of American grapevines are scarce. The objectives of this work were to (i) quantify the effects of downy mildew on gas exchange of *Vitis labrusca*, by the assessment of relationships between disease severity and photosynthesis and to determine the presence of virtual lesions (*sensu* Bastiaans, 1991), and (ii) to evaluate stomatal, diffusive and biochemical limitations of photosynthesis through measurements of gas exchange combined with measurements of chlorophyll fluorescence (*sensu* Farquhar et al., 1980; Sharkey et al., 2007). Grapevine plants of cv. Niagara Rosada were inoculated with different sporangia concentrations of *P. viticola* to obtain different levels of severity. Measurements of gas exchange and chlorophyll fluorescence were performed in diseased and healthy leaves, and data was related with severity of *P. viticola*. Photosynthetic responses to increasing intercellular CO_2 concentration were evaluated in grapevine leaves infected by *P. viticola*. The exponential negative model fitted well to the data of net photosynthetic rate (*A*) and the increase of disease severity (r^2 = 0.84). Values of *A* decreased 74 % in leaves with 50 % of downy mildew severity. A weak relation was observed between stomatal conductance and disease severity (r^2 = 0.47). According to Bastiaans model relative data of *A* (*P*x/*P*o) decreased with increased severity. The β-value was estimated by the model to be 2.8, indicating a moderate virtual lesion. *P*x/*P*o decreased by 83 % in leaves with 50 % of downy mildew severity, according to Bastiaans model. The maximum Rubisco carboxylation rate was observed in healthy plants. Estimated values of *A* maximum were 25.0 and 19.4 µmol m^{-2} s^{-1}, respectively, for healthy and diseased plants. The virtual lesions caused by *P. viticola* in susceptible cvs. Sangiovese (*V. vinifera*) and Niagara Rosada (*V. labrusca*) were similar. Differences in values of virtual lesions would imply genotypic differences in tolerance. The next steps of this work involve the determinations of β-values in controlled conditions in several *Vitis* spp. cultivars, including *V. vinifera* with resistance levels to downy mildew.

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Amplifier hosts as main inoculum sources of primary infection for tomato begomovirus epidemics in Brazil

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In some epidemics that have devastating consequences, as begomovirus disease of tomato in tropical and subtropical regions, the primary inoculum plays an important role in both epidemic onset and intensification. Despite their importance, little is known about the structure and behavior of epidemics of this type, i.e., polycyclic epidemics in which the primary inoculum has a continuous and dynamic role (Bergamin Filho et al., 2016). Management of such epidemics needs to address both the primary and secondary inoculum in an area-wide, regional basis. Control of secondary inoculum in many cases is not a problem and can be achieved by frequent insecticide sprays in the target crop; control of primary inoculum poses a considerable problem because insecticides applied in the target crop are inefficient and the main external sources of inoculum are unknown. Epidemics of *Tomato severe rugose virus* (ToSRV) in Brazil illustrate these points: (i) secondary infection is controlled by three insecticide sprays per week; (ii) despite this, epidemics occur frequently with high final incidence of symptomatic plants (> 70 %); (iii) external sources of inoculum are thought to be populations of susceptible weeds (acting as virus reservoir), but their epidemiological role is unknown. In this paper we propose, based on the frequent occurrence of epidemics even with efficient insecticide control of secondary inoculum, that the real source of primary inoculum must be stronger than the natural reservoir, i.e., we propose the existence in the agroecosystem of amplifier hosts (*sensu* Jones et al., 2013). By definition, an amplifier host is ideally an asymptomatic host that occurs in high density near the target host and supports both virus and vector. Soybean and common bean have these characteristics in tomato/ToSRV epidemics (Macedo et al., 2017a; 2017b). Recent observation by the authors (data not published) revealed that a soybean crop near harvesting, with estimated 51.2 % ToSRV-infected but asymptomatic plants (PCR analysis), appears to have been the disease amplifier alongside the tomato crop, as ToSRV incidence was 57 % of symptomatic plants, 50 days after transplanting.

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Tools for modelling plant disease epidemics with R

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The open-source program R not only provides a free and modern environment for statistical analyses and production of relevant graphics, but it can also be used for modelling plant disease epidemics. A variety of tools exist within R that can facilitate model development, even for scientists with little or no knowledge of simulation modelling. One example is the simulation model for potato late blight (caused by *Phytophthora infestans*), which was most recently adjusted for new genotypes (Andrade-Piedra et al., 2005). This model is available in the package 'agricolae' and can be accessed via the lateblight() function in that package. Other tools are available or can be developed depending on specific needs. If one needs to integrate (over time) various differential equations, this can be done within the 'deSolve' package with the ode() function. One relatively unique aspect of simulation of disease epidemics is the delays that can be used to mimic the latency or infectious periods. If fixed delays (without any dispersion) are sufficient, such as those in EPIMUL (Kampmeijer & Zadoks, 1977) these can also be found in 'deSolve' with the dede() function. If variable delays with dispersion are needed for the simulation model, then the dede() function is insufficient, and a function similar to the boxcar function (Goudriaan & Van Roermund, 1993) is needed. This function was originally written in FORTRAN to be called from a CSMP program. While R programs can use subroutines in FORTRAN, the original program listing of boxcar was an older variant of FORTRAN and was incompatible with R. A translation of the boxcar routine into R yields a function that mimics the original. A completely different class of models based on projection matrices can also be easily programmed within R (Caswell, 1997). These models are designed for organisms with distinct classes and do not rely on integration of differential or differential/difference equations. We have used this type of model to model rust development using data based on different spore types. While the 'popbio' package is designed to handle these projection matrices, R can easily handle the matix manipulation needs for these models, and elements of stochasticity can be implemented.

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Open ideas, data and code sharing: Epidemiologists should be in front!

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Botanical epidemiologists have long been leaders in using mathematical, statistical and computational approaches to tackle theoretical and applied research problems. Such skills always distinguished us from other plant pathology disciplines and naturally allowed us to bring together quantitative researchers (e.g. mathematicians, statisticians, programmers), something which has been beneficial to our area of research. The availability of increasing the amounts of data at scales from genomes to landscapes requires an even more diverse set of skills and enhanced ability to interact widely and advance the field. Additionally, donors, governments and journals are pushing for increased transparency and reproducibility (Bond-Lamberty et al., 2016). Because of this, an open approach to science is quickly becoming more accepted, including unconstrained access and sharing of scientific content, data collection and computer code. It is envisioned that fostering open science attitudes within our research communities will lead to improved reproducibility of the research, both in relation to the methods and the findings. Adopting reproducible research practices directly benefits us as researchers. Between complicated analyses, reviews and revisions and questions years later about the data that was collected or analysis that was conducted, it is extremely beneficial to be able to easily reproduce your work quickly and easily. Secondly, it is beneficial to the end-user or reader to be able to verify the validity of the methods used and recreate the analysis which helps with knowledge transfer. Lastly, sharing work openly and making it discoverable can lead to collaborations. While relatively few examples of reproducible research in plant pathology exist (Shah & Madden, 2004), this is now changing (Del Ponte, 2018; Duku et al., 2015; Sparks et al., 2018). To help facilitate this change, we founded the Open Plant Pathology community (Del Ponte & Sparks, 2018), which aims to foster relationships between researchers and promote open, transparent and reproducible research using shared data and reusable software. With our history of moving plant pathology forward using computational resources, botanical epidemiologists should be in front leading the way for plant pathology with these new methods.

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Pathway models for assessing the risk of invasion of plant pests and diseases; challenges and opportunities

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Invasive plant pests and diseases pose challenges to growers and governments worldwide. The current Xylella epidemic in southern Europe is just one of the great outbreaks that devastate farmer livelihoods and change cropping landscapes. Within the European Food Safety Authority, expert working groups strive to quantify the processes of entry, establishment, spread and impact using a variety of modelling approaches. Pathway modelling approaches are used to assess quantitatively the entry and establishment. Pathway models follow a trade flow from the country of origin to the point where the pest gets into contact with a host or habitat (Douma et al., 2016). The parameters of such models are estimated on the basis of statistical information on trade in combination with expert judgements on the prevalence of infection/infestation and the likelihood of transfer and establishment. The latter is informed by species distribution models. Expert knowledge elicitation is applied to translate trade data, scientific evidence and expert knowledge into estimates of model parameters. Uncertainty is assessed explicitly in the applied methods for expert knowledge elicitation at EFSA (EFSA Scientific Committee, 2018: a, b). Monte Carlo simulations are conducted with the resulting models to generate projections of future entry, establishment, spread and impact. Uncertainty in parameters is propagated in the simulations such that the projections are distributions. Scenario analyses are conducted to assess the effectiveness of risk management options implemented in the model framework. How useful and accurate are such model explorations? Are the results good enough for risk managers to act on them? Does quantification improve risk assessment and risk management? The talk will outline the conceptual framework for the risk assessment process, and present the use of expert knowledge elicitation and assessment of uncertainty to elaborate the conceptual framework into a quantitative model. Examples will be drawn from recent risk assessments at EFSA using this quantitative methodology.

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Multi-modeling approach for IPM

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Plant disease control has traditionally been based on calendar applications of fungicides to keep the plants constantly protected from fungal pathogens. Integrated pest management (IPM) is an important alternative to this traditional approach. Directive 128/2009/EC on the Sustainable Use of Pesticides makes IPM mandatory across Europe, with the goals of reducing the negative effects of pesticides on human health and the environment. IPM involves four types of decisions (Rossi et al., 2012). Type I decisions concern the selection of measures for the prevention and/or suppression of harmful organisms. Type II decisions concern whether and when plant protection actions are required. Type III decisions, which are made after growers have decided that crop protection is needed, concern the control measures to be used. When pesticides are used, they must be selected based on their effects both on target and non-target organisms as well as to prevent the development of pesticide resistance in the target population; they must also be applied at the lowest levels needed to achieve pest control. Type IV decisions concern the implementation of the management actions including adjustment of spray volume, sprayer speed, and spray timing during the day. Correct decision-making for IPM then requires the assessment of multiple risk factors. Plant disease models have been used to predict disease risk and support decisions about whether and when to protect crops based on environmental conditions. In addition to requiring information about disease risks, correct decision-making also requires answers to several questions. These include: Is the plant susceptible to infection? Is the plant protected by a previous fungicide application? Which fungicide should be used for the specific application? Which dose of the product should be used, and when should it be applied? Answering these questions requires a multiple modelling approach that includes models for plant disease, for plant growth and development (with consideration of disease resistance), and for the effects of fungicides. Decisions regarding whether and when it is necessary to protect the crop depend on the following risk factors: i) the risk of disease infection (as indicated by plant disease models); ii) plant susceptibility to the disease (as indicated by plant growth models); and iii) the residual efficacy of previous fungicide sprays (as indicated by fungicide models). A method of integrating these risk factors is needed, and one such method is the use of a fuzzy control system (FCS). Systems for defining the product dose and when the environmental conditions are suitable for application are also needed to complete the decision-making process. Crop-adapted spray application, for instance, makes it possible to obtain constant quantities of active ingredient per unit of leaf area throughout the growing season. Models evaluating the relationships between meteorological conditions, the timing of pesticide application, and pesticide efficacy are also available. Knowledge of the behaviour of products in relation to weather conditions can increase their efficacy and even serve as a tool for reducing the doses. Decision support systems for IPM should provide farmers with all of the information required for correct, multi-criteria decision-making.

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Modeling epidemics in seed systems to guide management strategies

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Seed systems are key to the global distribution of improved varieties and technologies, but too often serve as important conduits for the human-mediated dispersal of plant pathogens. In high-income countries the problem of seed transmitted pathogens has been largely mitigated by the commercialization and regulation of seed production through "certified" or "clean" seed programs. In most low-income countries, however, seed systems are local and informal, with seed largely of unknown quality. In these systems a majority of farmers keep seed from previous seasons, or obtain seed locally from neighbors, traders, or markets, with occasional instances of long-distance trade. We evaluate the vulnerability of seed networks to the spread of diseases, to identify strategies for disease management. Here we present results from studies of three informal to partially formal seed systems from low-income countries representing different spatial scales and survey methods: sweetpotato in Uganda (Andersen et al., 2018), potato in Ecuador (Buddenhagen et al., 2017), and potato in the Republic of Georgia. In Northern Uganda, sweetpotato vine multipliers were surveyed weekly over the course of the 2014 growing season, and this data was used to construct an adjacency matrix of seed movement. We modeled the introduction of a hypothetical seed-transmitted pathogen, and evaluated the influence of both epidemic starting point and quarantine treatments on epidemic progress. We evaluated centrality measures (betweenness, closeness, eigenvector, and degree) for their utility in the selection of risk-based monitoring locations. Findings indicate important villages in the region for monitoring. In Ecuador, a mixed formal and informal potato seed system was evaluated to identify key locations for disease management. Exponential random graph models (ERGMs) were applied to assess how well farmers participating in the seed system were served by it, and whether factors such as gender influenced farmers' roles in the system. In Georgia, a country plagued by potato yields among the lowest in the world, an expert elicitation was conducted in 2017 across a broad range of participants from the Georgian potato production sector. We present elicitation results along with a model of the current potato seed exchange network. Using ERGMs we modeled scenarios of spread for emerging diseases within the country as part of a risk assessment analysis. Several regions are at high risk of pathogen introduction throughout the country, in the absence of intervention. We present findings along with critical knowledge gaps for these types of seed system network analyses. This analysis framework can be applied to provide recommendations for a wide variety of seed systems.

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Evaluating regional management strategies for avocado laurel wilt

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Regional management strategies are critical for the long-term control of diseases that can spread rapidly and persist in the environment. Laurel wilt is an emerging threat to Lauraceae worldwide, and affects trees in both natural and agricultural ecosystems (Ploetz et al., 2017). The disease has spread quickly throughout the southeastern United States, and now heavily affects avocado growers in south Florida. The disease can kill avocado trees within two to four weeks of infection, and spreads rapidly via root-grafts within groves. Drawing on a combination of surveys and expert elicitation, we model the social and biophysical network of the avocado growers and groves in south Florida. We use these networks to simulate how social influences and cost structures can affect a grower's adoption of critical management techniques and suites of control strategies, potentially including roguing of infected trees and use of prophylactic fungicides. We also evaluate how different incentive structures and regulatory efforts can help manage disease, and how natural disasters will impact both the epidemic and the grower's ability to respond to the epidemic. The grower network includes a few highly influential and well-connected individuals who serve as grove managers for smaller growers. The grove network itself is highly connected due to the aggregation of many groves. Preliminary analyses suggest regulatory efforts that incentivize removal of diseased trees and discourage abandonment of laurel wilt-affected groves can help to reduce regional disease, and function more effectively than incentivizing or punitive regulations alone. Natural disasters (e.g., Hurricane Irma) may reduce overall disease if affected groves are promptly removed; however, changes in vector behavior and prevalence or reduced management infrastructure that occur afterwards may lead to increased disease. Understanding how the social network guiding management adoption influences disease is critical for developing strategies for regional disease suppression. Effective regional management of avocado laurel wilt will require coordination among growers, managers, regulators, and researchers.

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Machine learning for disease epidemiology of blueberry mummy berry

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Northern highbush blueberry (*Vaccinium corymbosum*) suffers severe economic losses in the US Pacific Northwest due to mummy berry, caused by the fungal pathogen *Monilinia vaccinii-corymbosi*. Intensive fungicide applications throughout the growing season are currently the sole strategy for control. Machine learning was used to develop a prediction model for ascospore release based on three environmental factors (Harteveld et al., 2017). If initial fungicide applications could be timed to coincide with release of ascospores and limit primary infections, the number of fungicide applications could be reduced. The aim of this study was to validate the prediction model and determine if accuracy of the model could be increased using additional environmental factors. The model was validated using an internal split dataset approach *in vivo*. Apothecial development and air and soil temperature, precipitation, soil moisture, leaf wetness, relative humidity and solar radiation were monitored in four fields (A,B,C and D) in northwestern Washington using in-field weather stations and WSU's AgWeathernet stations in 2017. To determine if computed environmental factors could increase accuracy of the model, additional factors incl. rolling temperature averages and cumulative days at factor thresholds were evaluated. Internal dataset validation showed 78 % accuracy. The accuracy of the *in-vivo* predictions were lower, with 61 % (field A), 73 % (B), 69 % (C) and 75 % (D). Our findings suggest overfitting to the dataset that was used to develop the model, field B and D. Implementing computed environmental factors such as rolling averages increased model accuracy by 5-10 %, illustrating that there is a strong time series effect which we are currently exploring using a multidimensional time series approach using deep learning techniques including LSTMs. The use of machine learning and deep learning for predictive modeling of plant diseases is a promising approach, but requires large datasets to achieve high accuracy on a larger geographical scale.

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Comparing models to predict invasive range of an unwanted organism: Myrtle rust (*Austropuccinia psidii*) in New Zealand

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Austropuccinia psidii causes myrtle rust (also known as guava rust, eucalypt rust and 'ohi'a rust) and is a worldwide threat to plant ecosystems containing species in the Myrtaceae. When *A. psidii* was first detected on mainland New Zealand in May 2017, the incursion response, co-managed by the Ministry for Primary Industries and Department of Conservation, required information on climatic suitability for establishment to help focus surveillance and organism managemnent activities. Although New Zealand climatic risk had previously been predicted using various ecological modelling platforms (e.g., MaxEnt, Hanna et al., 2012; Climex, Kriticos et al., 2013; Multi and Consensus models, Narouei-Khandan, 2014), the predictions were inconsistent in marginal risk areas and they provided no information about the seasonality of risk. We therefore used published information on *A. psidii* to develop a pathogen process model, called the Myrtle Rust Process Model (MRPM), to predict infection risk using near-real time, virtual weather data. These were generated by the New Zealand Convective Scale numerical weather model, with hourly time resolution and 1.5 km spatial resolution, provided by the National Institute of Water and Atmospheric Research Limited (Beresford et al., 2018). During the first year of disease surveillance, *A. psidii* was detected only in areas identified as high to very high risk by the MRPM. The detection of *A. psidii* in the northwest of the South Island was consistent with MRPM predictions, but not with those of the ecological models. MRPM was well suited to tactical surveillance, and ongoing comparison with pathogen presence data will determine its long term accuracy.

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Temperature response curve and distribution of the infection speed of ascospores of *Venturia inaequalis*

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In many apple production areas, fungicides are applied in relation to rain events that trigger ejection of ascospores of *Venturia inaequalis*, which are responsible for primary infections of apple scab. Although the temperature and leaf wetness requirements for infection of ascospores have been studied for over 80 years, the distribution of the infection speed within a population of ascospores was never studied. Consequently, computer programs designed to help growers time sprays either base recommendations on the fastest spores which lead to very conservative spray thresholds, or as is the case for RIMpro empirically derived a distribution function. Our objective was to improve the distribution function included in RIMpro. To estimate the distribution of speed; we inoculated potted apple trees with ascospores of *Venturia inaequalis* and placed them in infection chambers at different temperatures. Trees were gradually taken out, quickly dried, and then incubated in standard conditions until lesions were enumerated. The number of lesions increased with infection time for the different temperatures up to a plateau corresponding to the infection time of the slowest spores. The infection curve was best modelled using the monomolecular function starting at the minimum infection duration. At temperatures between 4 °C and 24 °C, nonlinear Yan heat units (equivalent to hours at 20.1 °C) best predicted the infection severity. Minimum infection occurred within 6 hours of leaf wetness, whereas half the spores resulted in lesions after 8 hours of wetness. Although our results match the minimum infection values used in RIMpro, it is possible that the newly derived infection distribution function will improve decisions under field conditions.

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Aerial dissemination of *Lasiodiplodia theobromae* and *L. pseudotheobromae pycnidiospores*

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Since 2013 branch dieback in mature trees and mortality of young plants were observed throughout Israel in avocado plantations. Two fungi, belonging to the Botryosphaeriaceae class, *Lasiodiplodia theobromae* (*LT*) and *L. pseudotheobromae* (*LPT*), were routinely isolated from symptomatic tissues. The fungi were identified according to their morphology and by using molecular markers. To verify the involvement of *LT* and *LPT* in the development of the symptoms, Koch's postulates were successfully completed. *LT* and *LPT* infect many fruit trees including avocado, causing pre- and post-harvest symptoms (Eskalen et al., 2013; Garibaldi et al., 2012). The teleomorph stage of *LT* and *LPT* was not found in Israel yet and it was believed that these pathogens spread by pycnidiospores, splashed to short distances by raindrops during rain events. This is the common dissemination mechanism of fungi belonging to the *Botryosphaeriaceae* and *Dioporthaceae* classes, such as *Septoria*, *Ascochyta*, *Diplodia* and others (Chen et al., 2014; Kimber et al., 2007; Phillips et al., 2013; Travadon et al., 2007). Observations made in commercial avocado plantations raised the hypothesis that *LT* and *LPT* pycnidiospores disperse aerially to long distances, even in dry, rainless days. The formation, dissemination and dispersal of *LT* pycnidiospores were examined in a series of controlled environment experiments. Artificially inoculated avocado stem-segments (10 cm long) bearing pycnidia were placed in high RH conditions. Cirri containing abundant numbers of pycnidiospores were secreted from the pycnidia and when dried-out, the pycnidiospores remained attached in long threads and easily disseminated aerially. Effects of RH and temperature on the formation and the effect of wind speed on the dispersal of the pycnidiospores were quantified in a wind tunnel. In addition, the diurnal dispersal of *LT* and *LPT* pycnidiospores in commercial avocado plantation was followed using Burkard spore traps. The results confirmed the hypothesis that *LT* and *LPT* pycnidiospores disperse aerially in dry, rainless days. This finding has significant consequences in understanding their pathogen epidemiology and developing means for its suppression.

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Epidemiology of post-harvest diseases of carrots in cold storage

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Carrot is an important root vegetable in Norway and is cold-stored up to eight months before consumption. However, carrots are faced with challenges from postharvest diseases, often resulting in high economic loss. In Norway, post-harvest carrot losses range from 10 to 40 % (Franke et al., 2013), and only 40 to 50 % of stored carrots are sold at the end of the storage period (Nærstad, 2015). About 50 % of the out-grading in the packing houses are due to infection of the root by pathogens (Bond, 2016). In the research project "OptiRoot" (Thomsen, 2018), a survey was conducted to determine the incidence of pre- and postharvest diseases of carrot. Carrots were grown in four regions, and in each region carrots from one field was stored in three different packinghouses. Disease assessments were carried out on foliage one week before harvest, on harvested roots at time of harvest and after storage for six months. In each cold store, four storage bins were arbitrarily selected, and 100 carrots were placed in each bin. In addition to disease assessment, temperature and relative humidity (RH) were monitored throughout the storage period in each of the 12 packinghouses included. Totally nine post-harvest fungal diseases were identified. There was a significant variation in disease incidence among and within regions ($p \leq 0.05$). Disease incidence was highly significant and positively correlated with storage degree hours, which is a measure of how much (in degrees) and for how long (in hours) the storage air temperature goes above the base temperature of 0 °C. For instance, in Rogaland County, carrots produced in the same field but stored in three different packinghouses resulted in significantly different disease incidence ($P = 0.02$). There were very few carrots with macroscopic disease symptoms at harvest. In Rogaland, disease incidence at harvest was 3 %, but after storage, it was 24, 33 and 48 % in the three storages Rog2, Rog1 and Rog3, respectively. The storage degree hours were 403, 2157 and 5556 for Rog2, Rog1 and Rog3, respectively. A regression analysis yielded a linear model: $Y = 22.69 + 0.0045X$, $R^2 = 99.9$ %; where Y is the disease incidence and X storage degree hours. The low disease incidence at harvest but high disease incidence after storage may imply that storage conditions play a significant role in creating conditions suitable for latent infections to develop and spread within the bins and packing houses. The variation among different regions and storage conditions clearly suggested that the soil conditions and agronomic practices implemented in the region, and temperature and humidity fluctuations within the storage house contributed to a higher abundance of some diseases. Therefore, post-harvest epidemiology and potential for prediction of storage diseases from cropping conditions in the field and storage conditions after harvest is important to minimize the high storage losses of carrots and economic loss in the carrot supply chain.

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Assisting peanut growers in reducing harvest losses in the presence of defoliation caused by leaf spot diseases

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The loss of leaf tissue through defoliation can adversely affect plant health, crop productivity and grower profitability, with effects being influenced by the severity of defoliation and the timing at which it occurs, depending on the system in question. Two such fungal diseases capable of eliciting premature canopy defoliation in peanut (*Arachis hypogaea*) are late and early leaf spot, respectively caused by *Cercosporidium personatum* and *Cercospora arachidicola*. Both diseases are important on a global scale, can be expensive to manage under common commercial settings and are more challenging to manage once infections become established. To explore the possibility of improving management recommendations in the presence of these leaf spots and quantify relationships of corresponding end-of-season defoliation and yield loss, meta-regression models were fitted to defoliation and yield data from peanut trials (19-year period) meeting established criteria. Slopes of proportion relative yield loss with increasing defoliation were estimated separately for runner (43 data sets) and Virginia (59 data sets) market type varieties. Results for runner-types indicated yield loss to linearly increase 2.3 to 3.0 % per 10 % increase in defoliation for levels up to approximately 95 % defoliation, after which the rate of loss increased more rapidly. Yield loss for Virginia-types was better described by an exponential function with a relative loss increase of 1.1 to 2.1 % of current loss levels per additional percent defoliation. To complement these results, separate meta-analytic models were fitted to trials with multiple harvest dates (20 data sets) and to applicable trials with multiple defoliation ratings (14 data sets) to obtain respective estimates of rate of relative yield increase towards a relative optimum from digging dates within 21 days of optimal relative yield (0.7 to 1.4 % per day) and potential logistic rate of defoliation progress (0.008 to 0.18 per day). While numerous factors remain important in mitigating overall losses, the integration of these findings should aid recommendations regarding digging under varying defoliation pressures and peanut maturities to assist in minimizing yield losses.

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Using optimal control theory to inform disease management at the landscape scale

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Sudden oak death (SOD), caused by *Phytophthora ramorum*, has been devastating oak and tanoak populations throughout California for decades. Although the disease is now very well-established, many valuable regions of forest resource remain uninfected. These include economically important timber production regions, as well as national parks important for biodiversity and tourism. The continued spread of the epidemic puts a number of such areas at risk. An important question is therefore how best to allocate limited detection and control resources to protect high value regions threatened by nearby disease. Landscape-scale mathematical models fitted to spread data provide a rational basis to inform how, where and when to control disease. A simulation model of SOD has previously been used to compare the performance of a range of control strategies to minimise total forest area lost to the disease. However, the complexity of models such as this, and the vast set of possible controls, let alone combinations of controls, means that only a small subset of all possible management strategies can ever be tested. A mathematical approach, optimal control theory, allows the very best control to be unambiguously identified. However, the complexity of the underpinning mathematics means that disease models must be highly simplified. Important features, perhaps most notably spatial heterogeneity and stochasticity, are almost always omitted. Despite these shortcomings, output from optimal control models can be used to provide alternative management strategies for testing on simulation models against researcher or policy-maker defined options. In addition to this, feedback control systems including model predictive control allow the use of the optimal control theory framework, whilst correcting for errors accumulated due to systematic model differences. This enables the insight from these mathematical models to be used in a structured and unbiased way, potentially providing novel management strategies for consideration. Here we show how optimal control theory and model predictive control can be used to help answer the question of where and when to allocate control resources to protect a high value region. We apply it to the example of Redwood National Park, which is threatened by a nearby disease outbreak in Redwood Creek. Using a model of SOD spreading into the national park through a buffer region, we show the optimal control strategies identified, as well as demonstrating the benefits of feedback mechanisms for handling parameter uncertainty and model complexity. We also look at extending the spatial complexity of the optimal control model to allow development of more highly resolved optimal strategies.

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Spatial-temporal pattern of plum leaf scald

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The Plum Leaf Scald (PLS) is the main disease of plum (*Prunus salicina*) in Brazil. This paper describes the temporal and spatial pattern of PLS under field conditions and the occurrence of sharpshooter vectors. Three commercial orchards were monitored in Parana State (southern Brazil), from 2010 to 2015 under subtropical climate. Incidence and severity of PLS were measured at each orchard. The number of sharpshooters (Hemiptera: Cicadellidae: Cicadellinae) were recorded at traps placed at two heights (0.50 and 1.9 m) aboveground. Descriptive analysis of the incidence was performed by the Kernel Smoothing method, spatial pattern with increased continuous information (distance) by the Average Distance Method and the spatial dependence structure according to the neighbouring of the plants by an autologistic model. The influence of summer pruning on the transmission of *Xylella fastidiosa* was also investigated, using *q*PCR technique. In the last year of assessments, the number of sharpshooters was similar among both trap heights, and increased from November to April, with a maximum observed in March. The progress of the PLS followed a polyetic epidemic from incidences increasing from 0 to 13, 6 to 85, 6.5 to 90.5 %, respectively, in the three orchards assessed. Aggregated patterns were detected by different methods, except with low incidences at the beginning of the epidemics. The autologistic model showed an increased risk of disease for trees with infected neighbouring trees within the same row at the same time of assessment, and an increase in the diagonal and between rows for years with high incidences (> 70 %) was observed. The dissemination by pruning shears was detected by *q*PCR after one year of incubation (2/24), but no symptoms were verified in the plants. The border effect, at the beginning of the epidemic, seems to be related to the entrance of the pathogen, possibly by vectors coming from external areas. The aggregate distribution of diseased plants suggests secondary dissemination by vectors, which could also be influenced by the management. Future investigations should be done to confirm these findings.

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Defoliation assessment of Asian grapevine leaf rust

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Plant-pathogenic fungi can establish different feeding relationships with their hosts: biotrophic, hemibiotrophic or necrotrophic. Usually, necrotrophic pathogens induce cell death and leaf senescence, but some biotrophic fungi are associated with senescence and defoliation, such as *Phakopsora pachyrhizi* (Asian soybean rust) and *Phakopsora euvitis* (Asian grapevine leaf rust). Grapevine early defoliation due to *P. euvitis* infection implies a decrease of photoassimilate production and, consequently, a reduction of yield and fruit quality. Defoliation is an important variable to be assessed in epidemiological studies. However, the relationship between disease severity and defoliation is rarely quantified in a leaf scale. For example, the intensity of Asian soybean rust in fungicide trials is evaluated either by disease severity or by plant defoliation, although no relationship has been established between Asian soybean rust severity and soybean defoliation. In this work, we compared two sample units ('shoots' *versus* 'leaves') to quantify the defoliation rate associated with the severity of Asian grapevine leaf rust. In order to obtain different levels of disease severity, grapevine plants of cv. Niagara Rosada (*Vitis labrusca*) were inoculated with different concentrations of a suspension of *P. euvitis* urediniospores (10^3, 10^4 or 10^5 urediniospores per mL) or water (control). Part of the vineyard was sprayed with fungicides to control grapevine rust and to evaluate natural leaf senescence. Every three or four days, the total number of leaves per shoot and the disease severity observed in each leaf were evaluated on 45 plants and 2 shoots per plant (90 shoots and 737 leaves in the first assessment). Shoots and leaves were grouped into 4 classes (0 to 0.09 %, 0.1 to 1 %, 1.1 to 5 %, and 5.1 to 12 %) according to the mean disease severity within the assessed period. For the sample unit 'shoots', defoliation rate was estimated by the logistic model (Madden et al., 2007) fitted to the number of leaves over time for each class of disease severity. Disease severity was estimated at 49 days post first symptoms. For the sample unit 'leaves', defoliation rate was calculated according to Willocquet et al. (2004) in the period of 49 to 62 days post first symptoms for each class of disease severity. This variable was expressed as the relative rate of defoliation (RRDEF). Disease severity was the mean of diseased area per leaf within this period. The rate of defoliation from sample unit 'shoots' was negatively correlated with the disease severity. The relative rate of defoliation from sample unit 'leaves' was directly correlated to disease severity.

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Weather conditions associated with mycotoxin accumulation in Norwegian oats

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High concentrations of the mycotoxins deoxynivalenol (DON), produced by *Fusarium graminearum*, and HT-2 and T-2, produced by *Fusarium langsethiae*, are occasionally detected in Norwegian oats. With the aim of predicting the risk of DON and HT-2 + T-2 accumulation, we identified weather conditions associated with mycotoxin accumulation in Norwegian oats. This work was performed in three parts: 1: A mathematical model to estimate developmental stages in oats (tillering, flowering, etc.) was developed based on growth stages recorded in oat fields and local weather data from their nearest weather station. 2: Weather summarisations within specific estimated oat developmental stages were calculated for oat fields with known mycotoxin concentrations in the harvested oat grain. To assess the association between weather conditions and mycotoxin accumulation, a Spearman rank correlation factor was calculated between mycotoxin concentrations and the weather summarisations within each developmental stage. 3: The most important weather variables identified were included in empirical models developed to predict the risk of DON and HT-2 + T-2 accumulation in harvested oats. The models were developed and evaluated using discriminant analysis with stepwise selection and leave-one-out cross-validation (Hjelkrem et al., 2017; Hjelkrem et al., 2018). Our data indicate that HT-2 + T-2 contamination in oats is influenced mostly by weather conditions both pre- and post-flowering, in contrast to DON which is influenced mostly by weather conditions from flowering onwards. Separate prognosis models should therefore be developed for DON and HT-2 + T-2 contamination in oats. The prediction models may be useful to the Norwegian cereal industry and authorities to identify grain lots with potential food safety problems.

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Epidemiological studies to improve the decision support system FusaProg

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Fusarium head blight (FHB) is one of the most important cereal diseases worldwide, caused by a complex of several *Fusarium* species. Infections frequently result in substantial yield losses and contamination of grains with health threatening mycotoxins. In field surveys, *Fusarium graminearum* (FG) and deoxynivalenol (DON) proved to be the most important FHB species and mycotoxin in Swiss winter wheat, respectively (Forrer et al., 2007; Vogelgsang et al., 2011; Vogelgsang et al. 2017). In addition, these studies confirmed that beside weather conditions and the presence of the pathogen, crop management factors, such as tillage and previous crop have an important impact on the FG infection risk and subsequent DON contamination. The internet based decision support system (DSS) FusaProg was developed to estimate field specific FG-infection and DON contamination risks in winter wheat and to support farmers to reduce DON contamination by improving the cropping system in winter wheat. The model considers and quantifies the effects of cropping factors, previous crops, soil and straw management, as well as the FG susceptibility of the variety (Musa et al., 2007). These driving variables are combined with the prevailing weather conditions and the growth stage in order to predict the DON content of a specific plot before harvest. To validate and quantify the effect of some crucial factors (e.g. straw management, weather rules), which are considered in the DSS FusaProg, epidemiological field experiments with spore traps were conducted. Results showed that different straw management methods clearly reduced the amount of deposited FG spores (30 up to 60 %) and FG infection rate (12 up to 18 %) in comparison with no-till treatments. FusaProg indicated crucial weather conditions one or two days before an increased number of FG spores were deposited. In 2017, epidemiological studies conducted in the frame of the H 2020 project "MycoKey", revealed a strong correlation between the number of FG spores, infection rate and DON contamination. These results will be used to further improve the DSS FusaProg.

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Dispersal of beneficial bacteria on plant leaf surfaces under protection

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Using biological control agents (BCAs) is an essential component of integrated pest and disease management. Despite much research on biocontrol of plant diseases, success in field crops has been limited with the success being mainly achieved in protected production systems. This lack of success is often attributed to the complex ecological processes involved in biocontrol. We are conducting a series of experiments to study ecological characteristics of several commercial BCAs, focusing on their dispersal and survival under natural conditions. This information will be valuable for predicting control efficacy (hence disease dynamics) in order to optimise application timings. Furthermore, the information will also be directly relevant to understanding disease dispersal under natural conditions. Here we report results from two studies investigating the dispersal of two beneficial bacteria under protected conditions. In one study, a commercial biocontrol product (Serenade), a formulated product of one specific *Bacillus subtilis* strain was applied to strawberry plants grown in open field and under protection. In the other study, Serenade and a beneficial Phyllobacterium were applied to lettuce plants in a glasshouse compartment. Next generation sequencing (NGS) technology was used to assess the dispersal of the two bacteria on plants. The dispersal of both bacteria was very limited under protection. In addition, there is a significant reduction in the BCA population size within 8 days of their application on the leaves that received the bacteria. The results suggested that limited dispersal is probably the main reason for its variable and often low control efficacy under field conditions. Thus to increase biocontrol efficacy, it is necessary to frequently apply BCAs with the application interval depending on the growth rate of target host tissues. Currently, studies are under way to determine the effect of climatic conditions on the survival of biocontrol organisms on leaf surfaces.

Revision of potato late blight risk forecasting in republic of Ireland

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Currently, the control of potato late blight (PLB) in Ireland is reliant on fungicides and given the potential yield loss and/or increased costs associated with controlling epidemics if initiated, fungicides are intensively applied prophylactically. Irish producers use, but do not necessarily rely on, warnings issued by Met Éireann (the Irish Meteorological Service). These warnings are based on the "Irish rules", a simple semi – empirical algorithm, originally developed in the 1950s (Bourke, 1953). Since then, significant changes have occurred in potato production systems relating to late blight epidemiology, the Irish *Phytophthora infestans* populations, and the development of more effective fungicides and resistant varieties (Kildea et al., 2010), yet the forecasting model has remained largely unchanged over this period. To address these shortcomings, a re-evaluation of the algorithm as currently employed for PLB forecasting is ongoing. Model parameters are refined using an empirical ROC analysis (Yuen et al., 1996). Data analysis and field validation of fixed and varying fungicide dose according to predicted risk, are indicating that the current algorithm and its decision thresholds need improvement. Under field conditions a modified version of the "Irish Rules", combined with a simple interpretation of the model outputs that match fungicide dose with late blight risk, have provided equivalent levels of late blight control as fungicide programs utilizing full dose. Late blight lesions were sampled from these trials to assess the impact of population structure on temporal disease dynamics under different treatments. Molecular characterization indicates population shift during the epidemics, where frequency of more aggressive pathogen strains is increasing, and resistant varieties break down at their mature phenological stages.

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Modelling Physical Mode of Action (PhMoA) of fungicides

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To optimize the timing of fungicide applications under an integrated pest management (IPM) strategy, the decision to apply a fungicide to control a plant disease should take into account several factors, including the effect of the last fungicide application (Rossi et al., 2012). Fungicide effect refers to the duration and degree of activity, and depend mainly on its physical mode of action (PMOA), that can be distinguished in pre-infection, post-infection, pre-symptom expression, and post-symptom activity. Fungicide effect is influenced also by other factors, such as the formulation of the fungicide, its dosage, the weather conditions and plant growth after application, and the multiple interactions among these factors. To optimize the timing of fungicide applications in relation to plant disease epidemics, researchers have constructed models that predict the dynamics of fungicide effect over time. These models have been developed mainly with an empirical approach, i.e., by fitting results obtained in field or laboratory experiments to mathematical equations. Polynomial models have been frequently used to describe the duration of fungicide control on different diseases (Caffi et al., 2018). However, the data reported for fungicide tests under field conditions could not be useful for understanding fungicide dynamics over time, because natural (and often repeated) infection periods make it impossible to separate pre-infection activity from post-infection and/or eradicant activity. To solve this problem, process-based (mechanistic) models can be developed. Those models consider the processes that determine fungicide dynamics and effects. This work describes a new process-based modelling approach to predict the temporal dynamic of fungicide effect. The model considers the effect of time, rainfall, biomass increase, and fungicide characteristics on fungicide efficacy dynamics. The model enables parameterization based on laboratory experiments, practical knowledge, and technical information. An example is presented on how the model was parameterized to evaluate the pre- and post-inoculation efficacy of copper-based fungicides against *Plasmopara viticola*, the causal agent of grape downy mildew. In laboratory experiments, fungicides were applied to grape leaves at different times before and after the *P. viticola* inoculation (Caffi et al., 2016). The model was validated by spraying the same fungicides in a commercial vineyard (northern Italy) at three times in 2016: ten leaves unfolded, pea-sized berries, and veraison. At 1, 3, 6, 9, or 12 d after each spray, 30 leaves were randomly collected, artificially inoculated with *P. viticola* sporangia in the laboratory, and then assessed for fungicide efficacy. The goodness of fit of the model to results from the field experiment suggests its ability to correctly predict fungicide efficacy.

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Incorporating host resistance in epidemiological models

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The cultivation of grapes resistant to main diseases has the potential to markedly reduce overall spraying with fungicides in viticulture. There is an increasing interest in the introduction in the European viticulture of those grape genotypes carrying genes (called *Rpv* genes) conferring partial resistance to *Plasmopara viticola*, the causal agent of downy mildew (DM). Resistant genotypes have been studied to understand the plant-pathogen relationships at molecular and physiological levels, but limited information is available on the DM epidemiology on resistant genotypes. Resistance to DM is currently assessed in the field or by laboratory assays based on sporulation intensity, which is only one of the epidemiological components involved in partial resistance. These measurements do not enable a careful characterisation of the resistant genotypes. A modelling approach can be a useful tool to guide phenotyping by integrating the effect of various components of resistance to DM. A systems-analytical approach was used to understand the effect of partially resistant grapevine genotypes on DM epidemics. A process-based model was designed by synthesizing the available knowledge on *P. viticola*-vine relationships. The flowchart was encoded using the STELLA® simulation software. The system under consideration was a grapevine plant surrounded by grapevine plants that are similar in terms of size, physiology development and disease. The proposed model easily explores the system in all the successive phases of the epidemic by focusing on the monocycle processes as components of the epidemic process: infection, latency, infectiousness, and removal. The model addresses the disease progress both on leaves and clusters, according to the dual epidemic caused by *P. viticola*, and accounts for growth and development of the crop. The relative resistance components (RRcs) were included as four coefficients affecting infection efficiency (RR_{IE}), latency period (RR_{LP}), infectious period (RR_{IP}), and sporulation rate (RR_{SP}). The individual and combined effects of these resistance components on the epidemic development were tested in a sensitivity analysis. Then, the model was implemented with parameter values for RRcs measured in controlled-environment experiments on sixteen resistant grape varieties carrying one or more *Rpv* genes. The model contributes in understanding the effect of each component of partial resistance on the epidemic development, making this modelling approach useful in better leading phenotyping studies. This approach is highly interesting for perennial crops where experiments are often difficult.

Predicting fungicide performance in the field from results of in vitro fungicide sensitivity assays

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In vitro fungicide sensitivity assays are useful for detecting shifts in the sensitivity of fungal pathogens to individual fungicides and evaluating resistance management strategies. The ability to accurately predict fungicide efficacy in the field and identify thresholds based on results of *in vitro* sensitivity assays would be of great value, especially for fungicides that exhibit quantitative resistance, but establishing these relationships has proven to be challenging. The relationship between *in vitro* assay results and fungicide performance has been investigated under greenhouse conditions or in the field for several pathosystems, with mixed results (Köller et al., 1997; Miller et al., 2002; Popko et al., 2012; Thomas et al., 2012). Management of pecan scab in the southeastern United States relies heavily on fungicides, and monitoring efforts have revealed significant reductions in sensitivity of the scab pathogen, *Venturia effusa*, to fungicides in several chemical classes, including demethylation inhibitors and organotins. An *in vitro* assay was developed to quantify fungicide sensitivity in *V. effusa* and provide growers with site-specific results (Seyran et al., 2010). In theory, these results could be used to tailor fungicide programs based on expected efficacy and avoid fungicides that are predicted to be ineffective. Experiments were recently conducted to determine the relationship between in vitro sensitivity of *V. effusa* to fentin hydroxide (TPTH) and tebuconazole (TEB) and efficacy of these fungicides in managing pecan scab under field conditions. Disease intensity was assessed on pecan trees receiving ten applications of TPTH, TEB, azoxystrobin, azoxystrobin + TEB, TPTH + TEB, or no fungicide (NTC) in 2016 and 2017. Sensitivity of *V. effusa* collected from treated and nontreated trees was assessed based on scab samples collected in June and September each year. Mean relative germination (RGe) on 30 µg/ml TPTH was 10.9 % and 40.9 % in 2016, and 4.2 % and 0.6 % in 2017. Mean relative growth (RGr) on 1 µg/ml TEB in 2016 was 45.5 % and 34.6 %, and 69.3 % and 56.3 % in 2017. Relative to the NTC, TPTH reduced scab with RGe values between 0.6 % and 40.9 %, but the level of control was not commercially acceptable. Compared with the NTC, TEB did not significantly reduce leaf scab in 2017 or nut scab in either year, indicating that an RGr value between 34.6 % and 69.3 % is likely to result in a control failure on TEB-treated trees. Research is currently underway to further refine sensitivity thresholds for effective scab control with these fungicides.

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Spatial variation and temporal dynamics of fungicide sensitivity in *Venturia effusa* within a pecan orchard

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Pecan scab, caused by *Venturia effusa*, is the most destructive disease of pecan in the southeastern United States. To manage scab, growers in Georgia typically make 7 to 15 fungicide applications per season, with the interval between sprays dependent on weather conditions. Fungicide resistance has been a historic problem in this pathogen, and recent fungicide sensitivity monitoring results revealed unexpected variation among samples of *V. effusa* collected from groups of randomly selected trees in the same orchard on the same day. Many epidemiological studies of fungicide resistance have examined changes in populations over time but few have identified spatial patterns of fungicide resistant individuals, despite the potential significance for resistance monitoring and overall disease management. Beginning in 2015, a three-year study was conducted to investigate the spatial and temporal variation in fungicide sensitivity of *V. effusa* at the landscape scale. An 18-ha commercial orchard block consisting of approximately 576 trees (predominantly of cv. Desirable), planted in a square pattern with approximately 18.3 m between trees in both directions was chosen for use in this study. The block was divided into 64 quadrats, each containing nine trees and in each year, approximately 50 leaflets exhibiting scab symptoms were collected from the lower canopy of the trees within each quadrat. Samples were collected on 22 June 2015, 20 June 2016, and 10 July 2017, when disease incidence was great enough to obtain an adequate sample. Fungicide sensitivity was assessed for propiconazole (PROP; 1 µg/ml), thiophanate-methyl (TPM; 5 µg/ml), or fentin hydroxide (TPTH; 30 µg/ml), using a bulk-spore assay described by Seyran et al. (2010). Sensitivity to all three fungicides varied significantly among the quadrats within years. Mean and standard deviation of percent relative growth for PROP were 15 and 34 % in 2015; 47 and 26 % in 2016; and 51 and 22 % in 2017. For TPM, mean and standard deviation of percent relative germination values were 45 and 24 % in 2015; 57 and 21 % in 2016; and 36 and 32 % in 2017. For TPTH, these values were 7 and 12 % in 2015; 13 and 8 % in 2016; and 7 and 14 % in 2017. Sensitivity to all three fungicides was significantly lower in 2016 than in 2015 but significantly greater for TPM and TPTH in 2017. Significant spatial autocorrelation was observed in sensitivity to PROP in 2017 (Geary's C = 0.8262, P < 0.0001) and to TPM in 2015 and 2017 (Geary's C = 0.9451, P = 0.0423; and Geary's C = 0.9318, P = 0.0110, respectively), suggesting clustering, but not for any other fungicide × year combination. Omnidirectional semivariograms were generated for each fungicide × year combination and spatial dependency was observed for both PROP and TPM in 2017. In both instances, the semivariance increased with distance within the orchard block; however, no sill was identified for either of these fungicide × year combinations, and thus the range of spatial dependence could not be estimated. Understanding the spatial and temporal variation in fungicide sensitivity within an orchard is important while designing sampling protocols for future sensitivity monitoring and may provide further insight into the spread of resistance in agricultural settings.

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Powdery mildews in controlled environment agriculture systems: The underestimated role of light

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Crop production under glass or polyethylene plastic is mostly associated with high value crops, such as strawberries, rose, cucurbits, and tomato. Powdery mildews are one of the most yield-reducing diseases of crops under covered production systems. Temperature and relative humidity have been discussed as the main drivers of powdery mildew development for many decades. Furthermore, control of powdery mildews is difficult, with pathogen populations rapidly becoming resistant to fungicides. Thus, there is a need for the development of alternative control strategies. Work in recent years has shown powdery mildew species to be highly sensitive to ultraviolet (UV) light exposure. Two experiments were set up to understand the effect of ultraviolet light on the epidemic progress of strawberry powdery mildew, caused by *Podosphaera aphanis*. In the first experiment, four treatments were tested; 1) ethylene tetrafluoroethylene (ETFE) plastic which blocks approximately 90% of solar UV-B light, 2) ETFE plastic which blocks approximately 10% of solar UV-B light, 3) a polyethylene plastic which blocks nearly 99% of solar UV light, and 4) a non-covered treatment. Foliar disease severity under all plastics was higher than in open field plots. Among plastic treatments, foliar severity and fruit disease incidence were highest under polyethylene and lowest under UV-transmitting ETFE. In the second UV experiment, a dense reflectorized hemicylindrical array of multiple UV fluorescent lamps pulled by a tractor was used to expose strawberry plants to a total UV energy of approximately 84.5 or 169 J m^{-2} 1 hr after sunset, either once or twice weekly. In the 2016-17 and 2017-2018 growing seasons, UV reduced foliar mildew severity up to 99% compared to the nontreated control, and provided greater suppression than a standard fungicide treatment. The lack of UV under certain plastics and greenhouse glass may markedly contribute to the environmental favorability for powdery mildews. Results will be presented to discuss the utility of UV light application for the control of strawberry powdery mildew that may have high potential to be applied across crops where powdery mildews are problematic.

Discontinuities in pathogen prevalence arising from non-additive interactions between genes or environmental factors

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In many cases the driver of pathosystem change is obvious: invasion, a new fungicide, and so on. But response may be delayed, and there are multiple examples of sudden transitions between two apparently stable states of a pathosystem where the driving force of the transition seems too small or ineffective to cause the change. One example is the development of fungicide resistance due to multiple interacting genes, in a species with some form of genetic recombination. If many loci are involved in a network of genes controlling a character, such as fungicide resistance, and they act additively, we expect a steady change in the character over time. However, the assumption of additivity is doubtful (Breen et al. 2012). Examples in which crosses between pathogen strains reveal non-additive interactions between multiple genes influencing fungicide resistance include Mavroeidi (2005) and Cordero Limon (2018). If alleles interact non-additively, with substantial epistasis, a sharp, rapid, change in resistance after a long delay may occur instead, as if the character was under single locus control but delayed. If the fully resistant phenotype is initially very rare, the delay may be very long. The delay increases with the number of genes involved, but approaches an asymptotic value; the delay and pattern of increase vary only moderately around a modal value. If virulence on a particular host has a similar multifactorial genetic architecture with strong epistasis, sudden transitions in prevalence on that host could be expected, without obvious proximate changes in environment or host geographic range. The strength of selection will presumably depend strongly on the proportion of the landscape on which any reproduction can take place; if this is large, the selective advantage to adapting to a new host will be reduced. If the resistance is effectively absolute at the start, then selection will be very slow or zero (because the additive genetic variance is effectively zero). There will be a waiting time until a successful simultaneous multiple mutant emerges, which is likely to be both long on average and very variable; the detail will depend not only on the pattern of epistasis and on the population size in the starting niche but on whether the variants are selectively neutral in the pathogen's starting niche. If the variant alleles are even slightly deleterious, then the waiting time for a host jump will be exponentially distributed with a mean which is inversely proportional to population size, the exponential of the mutation rate and the exponential of the number of genes which need to mutate to give a pathogenic phenotype on a new host (of the same or different species). The challenge for genetic engineers is to keep the mutation rate down and uncorrelated across inserted constructs and to use as many genes in a construct as possible, so that resistance breakdown is very unlikely. Analogous effects could occur when the response of a pathogen to host density is non-linear due to Allee effects, network structure (i.e. spatial pattern), or the mode of transmission between host patches. The detailed examples may carry implications for designing resilient farming systems.

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Fungal mating is not necessarily random as often assumed

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Understanding pathogen population structure and its dynamics is important for deploying cultivars to preserve resistance and manage diseases. Sexual recombination is one of the most important factors driving pathogen population dynamics. Random mating between compatible fungal strains is usually assumed, and this assumption has critical impacts on the reliability and accuracy of the predictions of the dynamics/spread of specific genes/traits within a population. Within the context of epidemiology, we are mainly concerned with the spread of genes that confer virulence against specific host resistance, and resistance against specific fungicides. Scab is one of most economically important diseases of apples worldwide. This disease is caused by the haploid ascomycete *Venturia inaequalis*. It has been assumed that sexual reproduction takes place on fallen leaves randomly between strains of opposite mating types in the winter, and mature ascospores are then released in the spring to initiate primary infections. Recently, we have obtained data from artificial inoculation and SSR-marker-based population variability studies, suggesting that mating between scab strains may not be as random as we often assumed. Whilst there appears to be random mating between strains from cultivars Bramley and Cox in the same orchard, the data strongly suggest a lack of recombination between strains from cultivars Bramley and Worcester in the same orchard. To investigate this apparent deviation from the expected 'random mating', we sequenced 24 strains from cultivars Cox, Bramley and Worcester from the same mixed orchard of ca. 50 years. We generated an annotated *V. inaequalis* whole genome sequence of 72 Mb in size, assembled into 238 contigs with 13871 predicted genes. Single Nucleotide Polymorphisms (SNPs) were called between all the isolates as well as cultivar specific "private" alleles. The scab populations isolated from cultivars Bramley and Worcester differed significantly, while Cox isolates were an admixture, supporting previous results. Given the number of total SNPs and private alleles in isolates from Bramley and Worcester, a higher or lower number of private alleles were present on contigs than expected under the assumption of random distribution of private alleles among total SNP alleles. Furthermore, within individual contigs these private alleles were much closer to each other than expected (i.e. spatially aggregated on the contig). This suggests that there is limited mating between isolates from Bramley and Worcester even though they were planted in the same orchard in a close proximity. This result could be explained by the hypothesis that sexual reproduction is initiated, at least predominantly, between isolates on the same leaf before leaf fall in the autumn. This could have wide ranging consequences on understanding population structure and disease management.

The role of spatial heterogeneity in the optimal deployment of host crop resistance genes for durable and effective disease control

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Maximising crop disease resistance durability in the presence of rapidly evolving pathogen populations is one of the major challenges in modern agricultural epidemiology. Resistance that maintains its effectiveness over long periods of time is crucial for achieving high crop yields, without resorting to the heavy use of expensive chemical pesticides and their associated environmental costs. This study uses a seasonal epidemiological model to explore the effect of explicit spatial heterogeneity, in the arrangement of fields planted with either susceptible or resistant cultivars, on landscape scale disease dynamics. The model features both wild-type and resistance breaking pathogen strains, and incorporates a localised reservoir inoculum, combined with the effects of within and between field transmission. We show that smaller scales of spatial heterogeneity drive lower epidemic intensities in the landscape over a wide range of eco-evolutionary timescales. This is due to an increase in the strength of dilution effects, or the proportion of inoculum that is wasted as it disperses onto the host cultivar where that pathogen strain has reduced relative fitness. This spatial suppression of epidemic intensities could be a viable strategy to maximise resistance durability and crop yields, however, its cost effectiveness will depend on the factors affecting the strength of the effect. These include the dispersal characteristics of the pathogen, the fitness costs associated with the resistance breaking trait, the efficacy of the host resistance gene, and the length of the timescale of interest. Some of these factors produce complex and unexpected trade-offs, driven by differing host-pathogen dynamics at different scales of spatial heterogeneity. These results in particular highlight the importance of studying the effect of genetics on landscape scale spatial dynamics within the host-pathogen disease system.

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